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                     GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on:          May 13, 2003, 01:11:58 ; Search time 2178 Seconds
                                            (without alignments)
                                            8074.403 Million cell updates/sec

Title:           US-10-003-354-3
Perfect score:   3713
Sequence:        1 attaacaggccgtggttagg..........aaactttaatgagttattta 3713

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6138095 seqs, 2368172464 residues

Total number of hits satisfying chosen parameters:      12276190

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_NA_New:*
                 1:  /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
                 2:  /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
                 3:  /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
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                 6:  /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
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                 11:  /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result              Query
   No.   Score     Match Length DB  ID                          Description
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     1    3713     100.0   3713  1  PCT-US02-38615-3             Sequence 3, Appli
     2    3713     100.0   3713  7  US-09-949-016-513            Sequence 513, App
     3    3577      96.3   3707  8  US-10-170-235-11868          Sequence 11868, A
     4  3575.8      96.3   3707 11   US-60-452-680-4962           Sequence 4962, Ap
     5  3575.8      96.3   3707 11   US-60-453-135-2839           Sequence 2839, Ap
     6  3575.8      96.3   3707 11   US-60-453-050-2839           Sequence 2839, Ap
     7    3125      84.2   3586  6  US-09-724-676-21450          Sequence 21450, A
     8    3125      84.2   3586  6  US-09-724-676A-21450         Sequence 21450, A
     9    3079      82.9   3622  6  US-09-724-676-21453          Sequence 21453, A
    10    3079      82.9   3622  6  US-09-724-676A-21453         Sequence 21453, A
    11    2821      76.0   3439  6  US-09-724-676-21451          Sequence 21451, A
    12    2821      76.0   3439  6  US-09-724-676A-21451         Sequence 21451, A
    13    2775      74.7   3475  6  US-09-724-676-21454          Sequence 21454, A
    14    2775      74.7   3475  6  US-09-724-676A-21454         Sequence 21454, A
    15    2679      72.2   2691  7  US-09-949-016-5869           Sequence 5869, Ap
    16    2014      54.2   2133  1  PCT-US02-38615-88            Sequence 88, Appl
    17    1852      49.9   2010  1  PCT-US02-38615-89            Sequence 89, Appl
    18  1833.4      49.4   5225  7  US-09-949-016-16351          Sequence 16351, A
    19  1715.4      46.2   2014  6  US-09-724-676-21452          Sequence 21452, A
    20  1715.4      46.2   2014  6  US-09-724-676A-21452         Sequence 21452, A
    21  1669.4      45.0   2050  6  US-09-724-676-21455          Sequence 21455, A
    22  1669.4      45.0   2050  6  US-09-724-676A-21455         Sequence 21455, A
    23  1656.4      44.6  19310  7  US-09-949-016-17611          Sequence 17611, A
    24  1656.4      44.6  54878  7  US-09-949-016-12255          Sequence 12255, A
    25  1623.4      43.7   1979  8  US-10-170-235-14486          Sequence 14486, A
    26  1524.8      41.1   2398  9  US-10-144-771-9741           Sequence 9741, Ap
    27  1458.4      39.3   1706  9  US-10-085-198-75             Sequence 75, Appl
    28  1329.2      35.8   1539  1  PCT-US03-02234-160           Sequence 160, App
    29  1329.2      35.8   1539  8  US-10-334-143-160            Sequence 160, App
    30   683.6      18.4   2209  9  US-10-144-771-9264           Sequence 9264, Ap
    31   674.4      18.2   5047 10   US-60-459-782-11             Sequence 11, Appl
    32   674.4      18.2   5047 11   US-60-427-982-11             Sequence 11, Appl
    33   674.4      18.2   5101  8  US-10-170-235-20637          Sequence 20637, A
c   34   674.4      18.2   5991  6  US-09-724-676-1858           Sequence 1858, Ap
c   35   674.4      18.2   5991  6  US-09-724-676A-1858          Sequence 1858, Ap
c   36   674.4      18.2   6464  6  US-09-724-676-1849           Sequence 1849, Ap
c   37   674.4      18.2   6464  6  US-09-724-676A-1849          Sequence 1849, Ap
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c   39   674.4      18.2   6485  6  US-09-724-676A-1854          Sequence 1854, Ap
c   40   674.4      18.2   6609  6  US-09-724-676-1844           Sequence 1844, Ap
c   41   674.4      18.2   6609  6  US-09-724-676A-1844          Sequence 1844, Ap
c   42   674.4      18.2   6796  6  US-09-724-676-1863           Sequence 1863, Ap
c   43   674.4      18.2   6796  6  US-09-724-676A-1863          Sequence 1863, Ap
    44   607.4      16.4   5159  1  PCT-US03-02234-111           Sequence 111, App
    45   607.4      16.4   5159  8  US-10-334-143-111            Sequence 111, App


                                ALIGNMENTS


RESULT 1
PCT-US02-38615-3
; Sequence 3, Application PC/TUS0238615
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Isis Pharmaceuticals, Inc.
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-
;  TITLE OF INVENTION:  KINASE,  I( EXPRESSION
;  FILE REFERENCE: RTSP-0444
;  CURRENT APPLICATION NUMBER: PCT/US02/38615
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 10/003,354
;  PRIOR FILING DATE: 2001-12-06
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
;   LENGTH: 3713
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (401)...(2050)
PCT-US02-38615-3

  Query Match            100.0%;  Score 3713;  DB 1;  Length 3713;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3713;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
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Qy         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
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Db         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
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Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
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Qy     301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
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Db     361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420

Qy     421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
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Qy     481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540
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Qy     541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600
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Qy     601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660
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Qy     661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720
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Db     661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720

Qy     721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780
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Qy     781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840
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Db     781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840

Qy     841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900
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Db     841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900

Qy     901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960
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Db     901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960

Qy     961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020
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Db     961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020

Qy    1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080
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Qy    1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140
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Qy    1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200
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Db    1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200

Qy    1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260
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Db    1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260

Qy    1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320
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Db    1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320

Qy    1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380
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Qy    1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGTA 1440
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Qy    1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620
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Qy    1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800

Qy    1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860
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Db    1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860

Qy    1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920
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Db    1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920

Qy    1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980
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Qy    1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040
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Db    1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040

Qy    2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100
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Qy    2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160
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Qy    2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220
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Db    2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220

Qy    2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280
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Qy    2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460
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Qy     2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520
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Db     2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520

Qy     2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580

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Qy     2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700
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Db     2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760

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Qy     2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880
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Qy     3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120
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Db     3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120

Qy     3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180
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Db     3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180

Qy     3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240

Qy     3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300

Qy     3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360

Qy     3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420

Qy     3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480

Qy     3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540

Qy     3541 TTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3541 TTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600

Qy     3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660

Qy     3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713

RESULT 2
US-09-949-016-513
; Sequence 513, Application US/09949016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 513
;   LENGTH: 3713
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-513

  Query Match             100.0%;  Score 3713;  DB 7;  Length 3713;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3713;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60

Qy       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120

Qy      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180

Qy      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240

Qy      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300

Qy      301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360

Qy      361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420

Qy      421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
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Qy    481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540

Qy    541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600

Qy    601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660

Qy    661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720

Qy    721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780

Qy    781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840

Qy    841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900

Qy    901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960

Qy    961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020

Qy   1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080

Qy   1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140

Qy   1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200

Qy   1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260

Qy   1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320

Qy   1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380

Qy   1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGTA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGTA 1440

Qy   1441 TTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGA 1500

Qy   1501 TGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATAT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATAT 1560

Qy   1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620

Qy   1621 AGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACG 1680

Qy   1681 GTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTC 1740

Qy   1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800

Qy   1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860

Qy   1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920

Qy   1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980

Qy   1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040

Qy   2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100

Qy   2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160

Qy   2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220

Qy   2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280

Qy   2281 CCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTAT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTAT 2340

Qy   2341 TGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCT 2400

Qy   2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460

Qy   2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520

Qy   2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580

Qy   2581 TTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAGA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAGA 2640

Qy   2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700

Qy  2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760

Qy  2761 CTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATC 2820
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 CTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATC 2820

Qy  2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880

Qy  2881 TCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTGG 2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 TCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTGG 2940

Qy  2941 TTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATT 3000
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 TTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATT 3000

Qy  3001 TTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGA 3060
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 TTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGA 3060

Qy  3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120

Qy  3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180

Qy  3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240

Qy  3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300

Qy  3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360

Qy  3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420

Qy  3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480

Qy  3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540

Qy  3541 TTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 TTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600

Qy  3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660

Qy  3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713


RESULT 3
US-10-170-235-11868
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; Sequence 11868, Application US/10170235
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
;  TITLE OF INVENTION:  TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
;  FILE REFERENCE: CL001380
;  CURRENT APPLICATION NUMBER: US/10/170,235
;  CURRENT FILING DATE:  2003-03-17
;  NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 11868
;   LENGTH: 3707
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-170-235-11868

  Query Match             96.3%;  Score 3577;  DB 8;  Length 3707;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 3663;  Conservative    0;  Mismatches   15;  Indels   37;  Gaps    4;

Qy     1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 87

Qy    61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 147

Qy   121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 207

Qy   181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 267

Qy   241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
         ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   268 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 327

Qy   300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 387

Qy   360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 447

Qy   420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 507

Qy   480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
         ||||                                ||||||||||||||||||||||||
Db   508 CCTC--------------------------------AGGTGCCTTATGCCTCTGGCATGC 535

Qy   540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   536 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 595

Qy   600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   596 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 655

Qy   660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   656 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 715

Qy   720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   716 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 775

Qy   780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    776 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 835

Qy    840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    836 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 895

Qy    900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    896 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 955

Qy    960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
          |||||||||||||||||||||||||||||||||||||||||    | |   |||
Db    956 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATG---GTAAGGGAGAGAGAAG 1012

Qy   1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 CACTTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1072

Qy   1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1132

Qy   1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1192

Qy   1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTGGATGCTGACA 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTGGATGCTGACA 1252

Qy   1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1312

Qy   1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1372

Qy   1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1432

Qy   1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1492

Qy   1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1552

Qy   1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1612

Qy   1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1672

Qy   1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1732

Qy   1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1733 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1792

Qy   1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1852

Qy   1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1853 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1912
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Qy   1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1913 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1972

Qy   1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1973 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2032

Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2033 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2092

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2093 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2152

Qy   2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2153 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2212

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2213 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2272

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2332

Qy   2340 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2333 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2392

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2452

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2512

Qy   2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2513 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2572

Qy   2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2632

Qy   2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2692

Qy   2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2752

Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2812

Qy   2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2872

Qy   2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2932

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2933 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2992
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Qy    2999 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2993 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3052

Qy    3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3053 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3112

Qy    3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3113 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3172

Qy    3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3173 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3232

Qy    3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3233 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3292

Qy    3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3293 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3352

Qy    3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3353 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3412

Qy    3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3413 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCTA 3472

Qy    3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3473 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3532

Qy    3539 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3533 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3592

Qy    3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3593 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3652

Qy    3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3653 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3707

RESULT 4
US-60-452-680-4962
; Sequence 4962, Application US/60452680
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  GRUPE, Andrew
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001450
;  CURRENT APPLICATION NUMBER: US/60/452,680
;  CURRENT FILING DATE:  2003-03-07
;  NUMBER OF SEQ ID NOS: 116213
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4962
;   LENGTH: 3707
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-452-680-4962

  Query Match             96.3%;  Score 3575.8;  DB 11;  Length 3707;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 3660;  Conservative    3;  Mismatches   15;  Indels   37;  Gaps    4;

Qy       1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 87

Qy      61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 147

Qy     121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 207

Qy     181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 267

Qy     241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     268 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 327

Qy     300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 387

Qy     360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 447

Qy     420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 507

Qy     480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
           ||||                                ||||||||||||||||||||||||
Db     508 CCTC--------------------------------AGGTGCCTTATGCCTCTGGCATGC 535

Qy     540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     536 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 595

Qy     600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     596 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 655

Qy     660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     656 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 715

Qy     720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     716 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 775

Qy     780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     776 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 835

Qy     840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     836 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 895

Qy     900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     896 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 955

Qy     960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
           |||||||||||||||||||||||||||||||||||||||||    | |   |||
Db     956 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATG---GTAAGGGAGAGAGAAG 1012

Qy    1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 CACTTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1072

Qy    1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     1073 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1132

Qy     1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db     1133 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCYA 1192

Qy     1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1193 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1252

Qy     1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1253 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1312

Qy     1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
            ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db     1313 TAATGGATTAYAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1372

Qy     1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1373 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1432

Qy     1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1433 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1492

Qy     1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1493 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1552

Qy     1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1553 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1612

Qy     1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1613 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1672

Qy     1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1673 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1732

Qy     1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1733 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1792

Qy     1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1793 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1852

Qy     1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1853 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1912

Qy     1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
            |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db     1913 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTRGTTGGAGAGA 1972

Qy     1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1973 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2032

Qy     2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2033 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2092

Qy     2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2093 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2152

Qy     2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db,    2153 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2212

Qy     2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2213 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2272

Qy     2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2273 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2332

Qy     2340 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2333 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2392

Qy     2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2393 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2452

Qy     2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2453 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2512

Qy     2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     2513 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2572

Qy     2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2573 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2632

Qy     2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2633 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2692

Qy     2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2693 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2752

Qy     2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2753 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2812

Qy     2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2813 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2872

Qy     2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2873 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2932

Qy     2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2933 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2992

Qy     2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2993 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3052

Qy     3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3053 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3112

Qy     3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3113 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3172

Qy     3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3173 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3232

Qy     3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3233 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3292
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Qy    3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3293 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3352

Qy    3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3353 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3412

Qy    3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3413 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3472

Qy    3479 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3473 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3532

Qy    3539 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3533 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3592

Qy    3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3593 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3652

Qy    3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3653 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3707


RESULT 5
US-60-453-135-2839
; Sequence 2839, Application US/60453135
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  IAKOUBOVA, Olga
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001456
;  CURRENT APPLICATION NUMBER: US/60/453,135
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2839
;   LENGTH: 3707
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-453-135-2839

  Query Match             96.3%;  Score 3575.8;  DB 11;  Length 3707;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 3660;  Conservative    3;  Mismatches   15;  Indels   37;  Gaps    4;

Qy       1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 87

Qy      61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 147

Qy     121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 207

Qy     181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 267

Qy     241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     268 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 327

Qy     300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 387

Qy     360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 447

Qy     420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 507

Qy     480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
           ||||                                ||||||||||||||||||||||||
Db     508 CCTC--------------------------------AGGTGCCTTATGCCTCTGGCATGC 535

Qy     540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     536 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 595

Qy     600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     596 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 655

Qy     660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     656 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 715

Qy     720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     716 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 775

Qy     780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     776 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 835

Qy     840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     836 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 895

Qy     900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     896 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 955

Qy     960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
           |||||||||||||||||||||||||||||||||||||||||    | |   |||
Db     956 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATG---GTAAGGGAGAGAGAAG 1012

Qy    1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 CACTTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1072

Qy    1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1132

Qy    1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1133 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCYA 1192

Qy    1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1252

Qy    1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1312

Qy    1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
           ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 TAATGGATTAYAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1372

Qy    1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1373 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1432

Qy   1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1492

Qy   1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1552

Qy   1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1612

Qy   1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1672

Qy   1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1732

Qy   1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1733 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1792

Qy   1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1852

Qy   1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1853 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1912

Qy   1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
          |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   1913 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTRGTTGGAGAGA 1972

Qy   1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1973 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2032

Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2033 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2092

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2093 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2152

Qy   2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2153 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2212

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2213 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2272

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2332

Qy   2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2333 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2392

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2452

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2512

Qy   2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2513 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2572

Qy   2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2632

Qy   2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2692

Qy   2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2752

Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2812

Qy   2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2872

Qy   2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2932

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2933 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2992

Qy   2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2993 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3052

Qy   3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3053 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3112

Qy   3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3113 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3172

Qy   3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3173 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3232

Qy   3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3233 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3292

Qy   3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3293 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3352

Qy   3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3353 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3412

Qy   3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3413 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3472

Qy   3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3473 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3532

Qy   3539 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3533 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3592
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Qy    3599 GCAACATTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3593 GCAACATTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3652

Qy    3659 TACAATATAAAAGTGATATATGGTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3653 TACAATATAAAAGTGATATATGGTTTAATGTAATAAACTTTAATGAGTTATTTA 3707

RESULT 6
US-60-453-050-2839
; Sequence 2839, Application US/60453050
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  APPLICANT:  LUKE, May
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001457
;  CURRENT APPLICATION NUMBER: US/60/453,050
;  CURRENT FILING DATE:  2003-03-10
;  NUMBER OF SEQ ID NOS: 82762
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2839
;   LENGTH: 3707
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-453-050-2839

  Query Match             96.3%;  Score 3575.8;  DB 11;  Length 3707;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 3660;  Conservative    3;  Mismatches   15;  Indels   37;  Gaps    4;

Qy       1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 87

Qy      61 TGCCTCGTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      88 TGCCTCGTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 147

Qy     121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 207

Qy     181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     208 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 267

Qy     241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     268 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 327

Qy     300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     328 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 387

Qy     360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     388 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 447

Qy     420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 507

Qy     480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
           ||||                                ||||||||||||||||||||||||
Db     508 CCTC--------------------------------AGGTGCCTTATGCCTCTGGCATGC 535

Qy     540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     536 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 595

Qy     600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGAGCC 659
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     596 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGAGCC 655

Qy     660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     656 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 715

Qy     720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     716 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 775

Qy     780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     776 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 835

Qy     840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     836 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 895

Qy     900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     896 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 955

Qy     960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
           |||||||||||||||||||||||||||||||||||||||||    | |   |||
Db     956 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATG---GTAAGGGAGAGAGAAG 1012

Qy    1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 CACTTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1072

Qy    1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1132

Qy    1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db    1133 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCYA 1192

Qy    1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1252

Qy    1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1312

Qy    1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
           ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 TAATGGATTAYAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1372

Qy    1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1373 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1432

Qy    1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1433 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1492

Qy    1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1493 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1552

Qy    1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1553 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1612

Qy    1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1613 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1672

Qy    1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     1673 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1732

Qy     1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1733 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1792

Qy     1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1793 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1852

Qy     1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1853 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1912

Qy     1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
            |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db     1913 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTRGTTGGAGAGA 1972

Qy     1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1973 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2032

Qy     2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2033 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2092

Qy     2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2093 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2152

Qy     2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2153 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2212

Qy     2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2213 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2272

Qy     2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2273 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2332

Qy     2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2333 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2392

Qy     2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2393 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2452

Qy     2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2453 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2512

Qy     2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     2513 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2572

Qy     2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
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Db     2573 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2632

Qy     2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
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Qy     2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
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Qy     2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
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Db     2753 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2812

Qy     2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
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Qy     2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
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Qy     2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
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Qy     2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
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Db     2993 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3052

Qy     3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
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Db     3053 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3112

Qy     3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178
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Db     3113 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3172

Qy     3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238
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Db     3173 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3232

Qy     3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298
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Db     3233 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3292

Qy     3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358
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Db     3293 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3352

Qy     3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
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Db     3413 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3472

Qy     3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
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Db     3473 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3532

Qy     3539 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
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Db     3533 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3592

Qy     3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
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Db     3593 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3652

Qy     3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
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Db     3653 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3707
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RESULT 7
US-09-724-676-21450
; Sequence 21450, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 21450
;   LENGTH: 3586
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-21450

  Query Match             84.2%;  Score 3125;  DB 6;  Length 3586;
  Best Local Similarity   92.5%;  Pred. No. 0;
  Matches 3435;  Conservative    0;  Mismatches    0;  Indels  280;  Gaps    3;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
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Db         38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy         61 TGCCTCGTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
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Db         98 TGCCTCGTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
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Db        158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
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Db        218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 337

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
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Db        338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
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Db        398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
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Db        458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
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Db        518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 577

Qy        540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
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Db        578 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 637

Qy        600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
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Db        638 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 697

Qy        660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
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Db        698 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 757

Qy        720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
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Db        758 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 817

Qy        780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
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Db        818 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 877

Qy        840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
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Db        938 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 997

Qy        960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
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Qy       1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
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Db       1058 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1117

Qy       1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
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Db       1118 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1177

Qy       1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
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Db       1178 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1237

Qy       1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
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Db       1238 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1297

Qy       1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
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Db       1298 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1357

Qy       1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
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Db       1358 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1417

Qy       1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
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Db       1418 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1477

Qy       1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
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Qy       1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
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Qy       1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
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Db       1598 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1657

Qy       1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
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Db       1658 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1717

Qy       1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
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Db       1718 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1777

Qy       1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
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Qy       1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
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Db       1838 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1897

Qy       1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
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Db       1898 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1957

Qy       1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
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Qy       1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2018 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2077
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Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
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Db   2078 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2137

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
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Db   2138 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2197

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Db   2198 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2257

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
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Db   2258 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2317

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
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Qy   2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
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Db   2378 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2437

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
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Db   2438 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2497

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
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Qy   2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
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Qy   2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
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Db   2738 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2797

Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
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Db   2798 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2857

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Db   2918 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2977

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
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Qy   2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
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Db   3038 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3097

Qy   3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
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Db   3098 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAG---------- 3147

Qy   3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178
Db   3148 ------------------------------------------------------------ 3147

Qy   3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238
Db   3148 ------------------------------------------------------------ 3147

Qy   3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298
Db   3148 ------------------------------------------------------------ 3147

Qy   3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358
Db   3148 ------------------------------------------------------------ 3147

Qy   3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
                                      ||||||||||||||||||||||||||||||||
Db   3148 ----------------------------CAAATAACTGTCTATATTAGACACCCCCAGCC 3179

Qy   3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3180 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3239

Qy   3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3240 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3299

Qy   3539 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3300 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3359

Qy   3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3360 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3419

Qy   3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3420 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3474


RESULT 8
US-09-724-676A-21450
; Sequence 21450, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21450
;   LENGTH: 3586
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-21450

  Query Match             84.2%;  Score 3125;  DB 6;  Length 3586;
  Best Local Similarity   92.5%;  Pred. No. 0;
  Matches 3435;  Conservative    0;  Mismatches    0;  Indels  280;  Gaps    3;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217
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Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGCGGGGAGGTGGCCCACAGA 299
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGCGGGGAGGTGGCCCACAGA 337

Qy    300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 577

Qy    540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 637

Qy    600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 697

Qy    660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 757

Qy    720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 817

Qy    780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 877

Qy    840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 937

Qy    900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 997

Qy    960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1057

Qy   1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1117

Qy   1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1177

Qy   1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1237

Qy   1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1297

Qy   1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1357

Qy   1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1417

Qy   1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1477

Qy   1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1537

Qy   1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1538 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1597

Qy   1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1657

Qy   1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1717

Qy   1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1718 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1777

Qy   1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1837

Qy   1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1838 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1897

Qy   1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1898 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1957

Qy   1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1958 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 2017

Qy   1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2018 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2077

Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2078 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2137

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2138 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2197

Qy   2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2198 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2257

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2258 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2317

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2318 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2377

Qy   2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2378 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2437

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2438 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2497

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2498 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2557

Qy   2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2558 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2617

Qy   2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2618 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2677

Qy   2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2678 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2737

Qy   2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2738 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2797

Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2798 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2857

Qy   2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2858 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2917

Qy   2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2918 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2977

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2978 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 3037

Qy   2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3038 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3097

Qy   3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3098 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAG---------- 3147

Qy   3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178

Db   3148 ------------------------------------------------------------ 3147

Qy   3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238

Db   3148 ------------------------------------------------------------ 3147

Qy   3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298

Db   3148 ------------------------------------------------------------ 3147

Qy   3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358

Db   3148 ------------------------------------------------------------ 3147

Qy   3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
                                      ||||||||||||||||||||||||||||||||
Db   3148 ----------------------------CAAATAACTGTCTATATTAGACACCCCCAGCC 3179

Qy   3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3180 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3239

Qy   3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3240 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3299

Qy   3539 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3300 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3359

Qy   3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3360 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3419

Qy   3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3420 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3474


RESULT 9
US-09-724-676-21453
; Sequence 21453, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21453
;   LENGTH: 3622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-21453

  Query Match             82.9%;  Score 3079;  DB 6;  Length 3622;
  Best Local Similarity   91.6%;  Pred. No. 0;
  Matches 3435;  Conservative    0;  Mismatches    0;  Indels  316;  Gaps    4;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 337

Qy    300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGA----------------------- 516
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Db     518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTCTTGGAAGCTAGACAGGATT 577

Qy     517 -------------GGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 563
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Db     578 CTTACATCTCATTGGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 637

Qy     564 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     638 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 697

Qy     624 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     698 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 757

Qy     684 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 743
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     758 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 817

Qy     744 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 803
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     818 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 877

Qy     804 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     878 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 937

Qy     864 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 923
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     938 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 997

Qy     924 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 983
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     998 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 1057

Qy     984 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1043
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1058 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1117

Qy    1044 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1118 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1177

Qy    1104 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1178 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1237

Qy    1164 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1238 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1297

Qy    1224 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1298 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1357

Qy    1284 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1358 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1417

Qy    1344 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1418 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1477

Qy    1404 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1463
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1478 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1537

Qy    1464 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1523
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1538 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1597

Qy    1524 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1583
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1598 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1657

Qy    1584 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1643
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1658 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1717

Qy    1644 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1703
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1718 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1777

Qy    1704 CAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCAT 1763
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1778 CAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCAT 1837

Qy    1764 CTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCT 1823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1838 CTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCT 1897

Qy    1824 CTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTG 1883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1898 CTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTG 1957

Qy    1884 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 1943
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1958 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 2017

Qy    1944 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 2003
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2018 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 2077

Qy    2004 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 2063
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2078 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 2137

Qy    2064 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2123
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2138 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2197

Qy    2124 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2183
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2198 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2257

Qy    2184 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2243
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Db    2258 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2317

Qy    2244 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2303
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2318 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2377

Qy    2304 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2363
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Db    2378 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2437

Qy    2364 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2423
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2438 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2497

Qy    2424 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2483
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2498 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2557

Qy    2484 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2543
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2558 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2617

Qy    2544 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TTTTTTTTTTTCTGAAAAAGGAAAAA 2602
           ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    2618 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTTTTTTTTTTCTGAAAAAGGAAAAA 2677

Qy    2603 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2678 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2737
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Qy    2663 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2722
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Db    2738 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2797

Qy    2723 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2798 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2857

Qy    2783 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2842
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Db    2858 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2917

Qy    2843 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2918 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2977

Qy    2903 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 2962
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Db    2978 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 3037

Qy    2963 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTGCTCTTCTCATCTTTT 3022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3038 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTGCTCTTCTCATCTTTT 3097

Qy    3023 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3098 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3157

Qy    3083 CAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAG 3142
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Db    3158 CAGACAGTCCATATCTGTGAGGCCAG---------------------------------- 3183

Qy    3143 ATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCCCTGTCTTCATGCAG 3202

Db    3184 ------------------------------------------------------------ 3183

Qy    3203 GGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTT 3262

Db    3184 ------------------------------------------------------------ 3183

Qy    3263 TCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGGGGCCTGGTATCTCAGGCAGATT 3322

Db    3184 ------------------------------------------------------------ 3183

Qy    3323 GTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGATAATATGTTAGCCCAT 3382

Db    3184 ------------------------------------------------------------ 3183

Qy    3383 ACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3442
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3184 ----CAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3239

Qy    3443 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTT 3502
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Db    3240 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTT 3299

Qy    3503 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTT 3562
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Db    3300 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTT 3359

Qy    3563 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3360 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3419

Qy    3623 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3682
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Db    3420 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3479

Qy    3683 TTTAATGTAATAAACTTTAATGAGTTATTTA 3713
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Db    3480 TTTAATGTAATAAACTTTAATGAGTTATTTA 3510
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RESULT 10
US-09-724-676A-21453
; Sequence 21453, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21453
;   LENGTH: 3622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-21453

  Query Match             82.9%;  Score 3079;  DB 6;  Length 3622;
  Best Local Similarity   91.6%;  Pred. No. 0;
  Matches 3435;  Conservative    0;  Mismatches    0;  Indels  316;  Gaps    4;

Qy       1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
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Db      38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy      61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
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Db     158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy     181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy     241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 337

Qy     300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy     360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy     420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
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Db     458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy     480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGA----------------------- 516
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Db     518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTCTTGGAAGCTAGACAGGATT 577

Qy     517 -------------GGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 563
                        |||||||||||||||||||||||||||||||||||||||||||||||
Db     578 CTTACATCTCATTGGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 637

Qy     564 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 623
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Db     638 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 697

Qy     624 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     698 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 757

Qy     684 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 743
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     758 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 817
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Qy   744 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 803
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   818 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 877

Qy   804 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 863
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Db   878 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 937

Qy   864 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 923
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Db   938 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 997

Qy   924 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 983
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Db   998 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 1057

Qy   984 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1043
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Db  1058 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1117

Qy  1044 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1103
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1118 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1177

Qy  1104 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1163
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Db  1178 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1237

Qy  1164 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1223
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1238 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1297

Qy  1224 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1283
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1298 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1357

Qy  1284 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1343
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1358 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1417

Qy  1344 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1403
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1418 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1477

Qy  1404 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1463
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1478 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1537

Qy  1464 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1523
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1538 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1597

Qy  1524 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1583
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1598 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1657

Qy  1584 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1643
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1658 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1717

Qy  1644 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1703
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1718 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1777

Qy  1704 CAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCAT 1763
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1778 CAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCAT 1837

Qy  1764 CTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCT 1823
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1838 CTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCT 1897

Qy  1824 CTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTG 1883
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1898 CTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTG 1957

Qy  1884 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 1943
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1958 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 2017

Qy  1944 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 2003
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2018 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 2077

Qy  2004 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 2063
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2078 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 2137

Qy  2064 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2123
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2138 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2197

Qy  2124 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2183
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2198 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2257

Qy  2184 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2243
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2258 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2317

Qy  2244 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2303
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2318 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2377

Qy  2304 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2363
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2378 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2437

Qy  2364 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2423
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2438 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2497

Qy  2424 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2483
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2498 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2557

Qy  2484 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2543
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2558 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2617

Qy  2544 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TTTTTTTTTTCTGAAAAAAGGAAAAA 2602
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  2618 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTTTTTTTTTCTGAAAAAAGGAAAAA 2677

Qy  2603 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2662
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2678 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2737

Qy  2663 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2722
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2738 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2797

Qy  2723 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2782
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2798 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2857

Qy  2783 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2842
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2858 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2917

Qy  2843 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2902
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2918 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2977

Qy  2903 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 2962
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2978 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 3037

Qy   2963 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTGCTCTTCTCATCTTTT 3022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3038 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTGCTCTTCTCATCTTTT 3097

Qy   3023 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3098 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3157

Qy   3083 CAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAG 3142
          ||||||||||||||||||||||||||
Db   3158 CAGACAGTCCATATCTGTGAGGCCAG---------------------------------- 3183

Qy   3143 ATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCCCTGTCTTCATGCAG 3202

Db   3184 ------------------------------------------------------------ 3183

Qy   3203 GGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTT 3262

Db   3184 ------------------------------------------------------------ 3183

Qy   3263 TCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGGGGCCTGGTATCTCAGGCAGATT 3322

Db   3184 ------------------------------------------------------------ 3183

Qy   3323 GTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGATAATATGTTAGCCCAT 3382

Db   3184 ------------------------------------------------------------ 3183

Qy   3383 ACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3184 ----CAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3239

Qy   3443 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTT 3502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3240 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTT 3299

Qy   3503 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTT 3562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3300 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTT 3359

Qy   3563 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3360 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3419

Qy   3623 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3420 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3479

Qy   3683 TTTAATGTAATAAACTTTAATGAGTTATTTA 3713
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Db   3480 TTTAATGTAATAAACTTTAATGAGTTATTTA 3510


RESULT 11
US-09-724-676-21451
; Sequence 21451, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21451
;   LENGTH: 3439
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-21451

  Query Match            76.0%;  Score 2821;  DB 6;  Length 3439;
  Best Local Similarity   88.5%;  Pred. No. 0;
  Matches 3288;  Conservative    0;  Mismatches    0;  Indels  427;  Gaps    4;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGCGGGGAGGTGGCCCACAGA 299
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGCGGGGAGGTGGCCCACAGA 337

Qy    300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 577

Qy    540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 637

Qy    600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 697

Qy    660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 757

Qy    720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 817

Qy    780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 877

Qy    840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 937

Qy    900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 997

Qy    960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1057

Qy   1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1058 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1117

Qy   1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1177

Qy   1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1237

Qy   1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1297

Qy   1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1357

Qy   1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1417

Qy   1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1477

Qy   1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1537

Qy   1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1538 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1597

Qy   1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1657

Qy   1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1717

Qy   1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1718 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCT--------------- 1762

Qy   1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799

Db   1763 ------------------------------------------------------------ 1762

Qy   1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859

Db   1763 ------------------------------------------------------------ 1762

Qy   1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
                      ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1763 ------------GCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1810

Qy   1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1811 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1870

Qy   1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1871 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 1930

Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1931 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 1990

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1991 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2050
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Qy   2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2051 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2110

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2111 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2170

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2171 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2230

Qy   2340 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2231 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2290

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2350

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2351 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2410

Qy   2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2411 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2470

Qy   2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2471 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2530

Qy   2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2531 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2590

Qy   2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2591 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2650

Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2651 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2710

Qy   2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2711 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2770

Qy   2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2771 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2830

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2831 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2890

Qy   2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 2950

Qy   3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAG---------- 3000

Qy   3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178

Db   3001 ------------------------------------------------------------ 3000

Qy   3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238

Db   3001 ------------------------------------------------------------ 3000
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Qy       3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298

Db       3001 ------------------------------------------------------------ 3000

Qy       3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358

Db       3001 ------------------------------------------------------------ 3000

Qy       3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
                                          ||||||||||||||||||||||||||||||||
Db       3001 ----------------------------CAAATAACTGTCTATATTAGACACCCCCAGCC 3032

Qy       3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3033 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCTA 3092

Qy       3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3093 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3152

Qy       3539 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3153 TGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3212

Qy       3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3213 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3272

Qy       3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3273 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3327


RESULT 12
US-09-724-676A-21451
; Sequence 21451, Application US/09724676A
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21451
;   LENGTH: 3439
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-21451

  Query Match             76.0%;  Score 2821;  DB 6;  Length 3439;
  Best Local Similarity   88.5%;  Pred. No. 0;
  Matches 3288;  Conservative    0;  Mismatches    0;  Indels  427;  Gaps    4;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 97

Qy         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 337

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 577

Qy        540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 637

Qy        600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 697

Qy        660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 757

Qy        720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 817

Qy        780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 877

Qy        840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        878 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 937

Qy        900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        938 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 997

Qy        960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1057

Qy       1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1058 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1117

Qy       1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1177

Qy       1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1237

Qy       1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1238 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1297

Qy       1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1298 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1357

Qy       1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1358 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1417
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Qy    1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1418 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1477

Qy    1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1478 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1537

Qy    1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1538 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1597

Qy    1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1598 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1657

Qy    1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1658 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1717

Qy    1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
           |||||||||||||||||||||||||||||||||||||||||||||
Db    1718 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCT--------------- 1762

Qy    1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799

Db    1763 ------------------------------------------------------------ 1762

Qy    1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859

Db    1763 ------------------------------------------------------------ 1762

Qy    1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTACCTCAGACTCCACCTTTGG 1919
                       ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1763 ------------GCGTTCACCTTGGTCGTCCTGATGTTTACCTCAGACTCCACCTTTGG 1810

Qy    1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1811 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1870

Qy    1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1871 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 1930

Qy    2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1931 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 1990

Qy    2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1991 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2050

Qy    2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2051 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2110

Qy    2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2111 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2170

Qy    2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2171 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2230

Qy    2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2231 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2290

Qy    2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2291 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2350

Qy    2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2351 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2410

Qy    2520 CTCTGTAAAGGTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    2411 CTCTGTAAAGGTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2470

Qy    2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2471 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2530

Qy    2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2531 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2590

Qy    2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2591 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2650

Qy    2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2651 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2710

Qy    2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2711 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2770

Qy    2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2771 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2830

Qy    2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2831 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2890

Qy    2999 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 3058
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2891 TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAA 2950

Qy    3059 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTT 3118
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2951 GAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAG---------- 3000

Qy    3119 CTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATG 3178

Db    3001 ------------------------------------------------------------ 3000

Qy    3179 TCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCT 3238

Db    3001 ------------------------------------------------------------ 3000

Qy    3239 CCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAG 3298

Db    3001 ------------------------------------------------------------ 3000

Qy    3299 GGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCC 3358

Db    3001 ------------------------------------------------------------ 3000

Qy    3359 TGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCC 3418
                                       ||||||||||||||||||||||||||||||||
Db    3001 ----------------------------CAAATAACTGTCTATATTAGACACCCCCAGCC 3032

Qy    3419 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3033 AGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTA 3092

Qy    3479 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3093 TTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTC 3152

Qy    3539 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3598
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3153 TGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAA 3212

Qy   3599 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3213 GCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAA 3272

Qy   3659 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273 TACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3327


RESULT 13
US-09-724-676-21454
; Sequence 21454, Application US/09724676
; GENERAL INFORMATION:
;  APPLICANT: Compugen LTD
;  TITLE OF INVENTION: Variants of alternative splicing
;  FILE REFERENCE: 129181.4 Compugen
;  CURRENT APPLICATION NUMBER: US/09/724,676
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21454
;   LENGTH: 3475
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676-21454

  Query Match             74.7%;  Score 2775;  DB 6;  Length 3475;
  Best Local Similarity   87.7%;  Pred. No. 0;
  Matches 3288;  Conservative    0;  Mismatches    0;  Indels  463;  Gaps    5;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 337

Qy    300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGA----------------------- 516
          |||||||||||||||||||||||||||||||||||||
Db    518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTCTTGGAAGCTAGACAGGATT 577

Qy    517 -------------GGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 563
                       |||||||||||||||||||||||||||||||||||||||||||||||
Db    578 CTTACATCTCATTGGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 637

Qy    564 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 697

Qy    624 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 757

Qy    684 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 817

Qy    744 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 877

Qy    804 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 937

Qy    864 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 997

Qy    924 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 1057

Qy    984 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1117

Qy   1044 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1118 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1177

Qy   1104 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1178 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1237

Qy   1164 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1238 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1297

Qy   1224 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1298 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1357

Qy   1284 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1358 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1417

Qy   1344 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1418 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1477

Qy   1404 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1478 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1537

Qy   1464 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1538 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1597

Qy   1524 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1657

Qy   1584 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1658 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1717

Qy   1644 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1718 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1777

Qy   1704 CAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCAT 1763
          ||||||||||||||||||||
Db   1778 CAGTATTTAAGAAGATTCCCT--------------------------------------- 1798

Qy   1764 CTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCT 1823

Db   1799 ------------------------------------------------------------ 1798

Qy   1824 CTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTG 1883
                                                          ||||||||||||
Db   1799 ------------------------------------------------GCGTTCACCTTG 1810

Qy   1884 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 1943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1811 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 1870

Qy   1944 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 2003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1871 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 1930

Qy   2004 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 2063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1931 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 1990

Qy   2064 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1991 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2050

Qy   2124 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2051 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2110

Qy   2184 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2111 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2170

Qy   2244 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2171 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2230

Qy   2304 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2231 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2290

Qy   2364 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2350

Qy   2424 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2351 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2410

Qy   2484 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2411 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2470

Qy   2544 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TTTTTTTTTTCTGAAAAAAGGAAAAA 2602
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2471 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTTTTTTTTTCTGAAAAAAGGAAAAA 2530

Qy   2603 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2531 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2590

Qy   2663 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2591 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2650

Qy   2723 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2651 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2710

Qy   2783 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2711 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2770

Qy   2843 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2771 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2830

Qy   2903 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 2962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2831 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 2890

Qy   2963 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTT 3022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTT 2950

Qy   3023 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3010

Qy   3083 CAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAG 3142
          ||||||||||||||||||||||||||
Db   3011 CAGACAGTCCATATCTGTGAGGCCAG---------------------------------- 3036

Qy   3143 ATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCCCTGTCTTCATGCAG 3202

Db   3037 ------------------------------------------------------------ 3036

Qy   3203 GGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTT 3262

Db   3037 ------------------------------------------------------------ 3036

Qy   3263 TCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGGGGCCTGGTATCTCAGGCAGATT 3322

Db   3037 ------------------------------------------------------------ 3036

Qy   3323 GTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGATAATATGTTAGCCCAT 3382

Db   3037 ------------------------------------------------------------ 3036

Qy   3383 ACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3037 ----CAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3092

Qy   3443 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTCATAATTTACTATTT 3502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3093 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTCATAATTTACTATTT 3152

Qy   3503 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTT 3562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3153 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTT 3212

Qy   3563 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3213 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3272

Qy   3623 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3332

Qy   3683 TTTAATGTAATAAACTTTAATGAGTTATTTA 3713
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Db   3333 TTTAATGTAATAAACTTTAATGAGTTATTTA 3363
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RESULT 14
US-09-724-676A-21454
; Sequence 21454, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen

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;  CURRENT APPLICATION NUMBER: US/09/724,676A
;  CURRENT FILING DATE:  2000-11-28
;  NUMBER OF SEQ ID NOS: 97222
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21454
;   LENGTH: 3475
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-724-676A-21454

  Query Match             74.7%;  Score 2775;  DB 6;  Length 3475;
  Best Local Similarity   87.7%;  Pred. No. 0;
  Matches 3288;  Conservative    0;  Mismatches    0;  Indels  463;  Gaps    5;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 97

Qy         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 157

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 217

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 277

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        278 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 337

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 397

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 457

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 517

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGA----------------------- 516
              |||||||||||||||||||||||||||||||||||||
Db        518 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTCTTGGAAGCTAGACAGGATT 577

Qy        517 -------------GGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 563
                           |||||||||||||||||||||||||||||||||||||||||||||||
Db        578 CTTACATCTCATTGGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAGAA 637

Qy        564 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        638 GTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGGTG 697

Qy        624 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 683
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGATG 757

Qy        684 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 743
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        758 TCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAACC 817

Qy        744 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        818 TGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCC 877

Qy        804 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        878 GCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTG 937

Qy        864 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        938 AGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCG 997

Qy        924 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        998 ACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGC 1057

Qy        984 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1058 TTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTATG 1117

Qy       1044 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1118 GACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTT 1177

Qy       1104 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1178 TACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGC 1237

Qy       1164 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1238 GGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTAC 1297

Qy       1224 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1298 AAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCC 1357

Qy       1284 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1343
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1358 TGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGT 1417

Qy       1344 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1403
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1418 CAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTCAG 1477

Qy       1404 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1478 TTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCATCC 1537

Qy       1464 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1538 AGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTG 1597

Qy       1524 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1598 CCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGT 1657

Qy       1584 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1658 CTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACA 1717

Qy       1644 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1718 CTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACA 1777

Qy       1704 CAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCAT 1763
              |||||||||||||||||||||
Db       1778 CAGTATTTAAGAAGATTCCCT--------------------------------------- 1798

Qy       1764 CTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCT 1823

Db       1799 ------------------------------------------------------------ 1798

Qy       1824 CTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTG 1883
                                                              ||||||||||||
Db       1799 ------------------------------------------------GCGTTCACCTTG 1810

Qy       1884 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 1943
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1811 GTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTA 1870
```

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Qy   1944 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 2003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1871 TTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTA 1930

Qy   2004 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 2063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1931 CAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCA 1990

Qy   2064 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1991 GAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAG 2050

Qy   2124 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2051 CAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAG 2110

Qy   2184 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2243
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2111 CTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGG 2170

Qy   2244 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2171 GCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGT 2230

Qy   2304 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2363
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2231 ACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATT 2290

Qy   2364 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 CTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTA 2350

Qy   2424 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2483
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2351 GGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTT 2410

Qy   2484 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2411 CTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATA 2470

Qy   2544 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TTTTTTTTTTCTGAAAAAAGGAAAAA 2602
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   2471 AGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTTTTTTTTTCTGAAAAAAGGAAAAA 2530

Qy   2603 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2531 GCACACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGAT 2590

Qy   2663 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2591 GCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATT 2650

Qy   2723 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2651 GCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTG 2710

Qy   2783 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2711 AAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCA 2770

Qy   2843 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2771 GCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATA 2830

Qy   2903 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 2962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2831 GTAATTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGAC 2890

Qy   2963 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTT 3022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2891 TTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTT 2950

Qy   3023 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2951 CCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAA 3010

Qy   3083 CAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAG 3142
          ||||||||||||||||||||||||||
Db   3011 CAGACAGTCCATATCTGTGAGGCCAG---------------------------------- 3036

Qy   3143 ATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCCCTGTCTTCATGCAG 3202

Db   3037 ------------------------------------------------------------ 3036

Qy   3203 GGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTT 3262

Db   3037 ------------------------------------------------------------ 3036

Qy   3263 TCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGGGGCCTGGTATCTCAGGCAGATT 3322

Db   3037 ------------------------------------------------------------ 3036

Qy   3323 GTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGATAATATGTTAGCCCAT 3382

Db   3037 ------------------------------------------------------------ 3036

Qy   3383 ACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3037 ----CAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCT 3092

Qy   3443 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTCATAATTTACTATTT 3502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3093 GCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTCATAATTTACTATTT 3152

Qy   3503 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGGAGGGAATATTT 3562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3153 ATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGGAGGGAATATTT 3212

Qy   3563 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3213 GAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACT 3272

Qy   3623 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3273 ATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGT 3332

Qy   3683 TTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||
Db   3333 TTTAATGTAATAAACTTTAATGAGTTATTTA 3363

RESULT 15
US-09-949-016-5869
; Sequence 5869, Application US/09949016
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5869
;   LENGTH: 2691
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-5869

  Query Match             72.2%;  Score 2679;  DB 7;  Length 2691;
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Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2690;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy     1024 TTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGAT 1083
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 TTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGAT 60

Qy     1084 TGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAA 1143
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAA 120

Qy     1144 AGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATT 1203
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATT 180

Qy     1204 TAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTA 1263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTA 240

Qy     1264 CAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAAT 1323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAAT 300

Qy     1324 GGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAG 1383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAG 360

Qy     1384 CAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTC 1443
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTC 420

Qy     1444 CACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGA 1503
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGA 480

Qy     1504 CCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGG 1563
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGG 540

Qy     1564 CATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGC 1623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGC 600

Qy     1624 CCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTT 1683
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTT 660

Qy     1684 CCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAA 1743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 CCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAA 720

Qy     1744 AAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCAT 1803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 AAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCAT 780

Qy     1804 TACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGT 1863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 TACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGT 840

Qy     1864 GGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGA 1923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 GGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGAGGA 900

Qy     1924 AATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTT 1983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTT 960

Qy     1984 GCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCAC 2043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCAC 1020

Qy     2044 CCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAA 2103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAA 1080

Qy     2104 GATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAG 2163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAG 1140

Qy     2164 TGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCC 2223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTCTCC 1200

Qy     2224 TTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCT 2283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 TTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCCCCT 1260

Qy     2284 CCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGA 2343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 CCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGA 1320

Qy     2344 ATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTC 2403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 ATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTC 1380

Qy     2404 TTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGC 2463
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGC 1440

Qy     2464 ACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCT 2523
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 ACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCT 1500

Qy     2524 GTAAAGGTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TTTTTT 2582
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              Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

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; Sequence 9257, Application PC/TUS0225766
; GENERAL INFORMATION:
;  APPLICANT: GENE LOGIC, INC.
;  APPLICANT:  MUNGER, William E
;  APPLICANT:  FAULK, Ronald
;  APPLICANT:  SUN, Hongwei
;  APPLICANT:  SASAI, Hitoshi
;  APPLICANT:  WAGA, Iwao
;  APPLICANT:  YAMAMOTO, Jun
;  TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
;  FILE REFERENCE: 44921-5068-WO
;  CURRENT APPLICATION NUMBER: PCT/US02/25766
;  CURRENT FILING DATE:  2002-08-14
;  PRIOR APPLICATION NUMBER: US 60/311,837
;  PRIOR FILING DATE: 2001-08-14
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;   OTHER INFORMATION: Genbank Accession No. U78575
PCT-US02-25766-9257

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Db        601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660

Qy        661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720

Qy        721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780

Qy        781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840

Qy        841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900

Qy        901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960

Qy        961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020

Qy       1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080

Qy       1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140

Qy       1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200

Qy       1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260

Qy       1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320

Qy   1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380

Qy   1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGTA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGTA 1440

Qy   1441 TTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGA 1500

Qy   1501 TGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATAT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATAT 1560

Qy   1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620

Qy   1621 AGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACG 1680

Qy   1681 GTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTC 1740

Qy   1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800

Qy   1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860

Qy   1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920

Qy   1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980

Qy   1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040

Qy   2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100

Qy   2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160

Qy   2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220

Qy   2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280

Qy   2281 CCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTAT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTAT 2340

Qy   2341 TGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCT 2400

Qy   2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460

Qy   2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520

Qy   2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580

Qy   2581 TTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAGA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAGA 2640

Qy   2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700

Qy   2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760

Qy   2761 CTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATC 2820

Qy   2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880

Qy   2881 TCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTGG 2940

Qy   2941 TTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATT 3000

Qy   3001 TTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGA 3060

Qy   3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120

Qy   3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180

Qy   3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240

Qy   3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300

Qy   3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360

Qy   3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420

Qy   3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
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Qy   3481 TTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 TTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540

Qy   3541 TTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600

Qy   3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660

Qy   3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713


RESULT 2
US-10-003-354-3
; Sequence 3, Application US/10003354
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0348
;  CURRENT APPLICATION NUMBER: US/10/003,354
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 3
;   LENGTH: 3713
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (401)...(2050)
US-10-003-354-3

  Query Match            100.0%;  Score 3713;  DB 38;  Length 3713;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3713;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300

Qy    301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360

Qy    361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420

Qy    421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
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Qy    481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540

Qy    541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600

Qy    601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660

Qy    661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720

Qy    721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780

Qy    781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840

Qy    841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900

Qy    901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960

Qy    961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020

Qy   1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080

Qy   1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140

Qy   1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200

Qy   1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260

Qy   1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320

Qy   1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380

Qy   1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTA 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTA 1440

Qy   1441 TTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGA 1500

Qy   1501 TGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATAT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATAT 1560
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Qy   1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAA 1620

Qy   1621 AGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 AGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACG 1680

Qy   1681 GTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTC 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTC 1740

Qy   1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTG 1800

Qy   1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGA 1860

Qy   1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGGA 1920

Qy   1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGAC 1980

Qy   1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTT 2040

Qy   2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATCC 2100

Qy   2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAAG 2160

Qy   2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCTC 2220

Qy   2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 TCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATCC 2280

Qy   2281 CCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTAT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTAT 2340

Qy   2341 TGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGCT 2400

Qy   2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGCT 2460

Qy   2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAATC 2520

Qy   2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTT 2580

Qy   2581 TTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAGA 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAGA 2640

Qy   2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTT 2700

Qy   2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCT 2760

Qy   2761 CTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTATC 2820

Qy   2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAA 2880

Qy   2881 TCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTGG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTGG 2940

Qy   2941 TTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATT 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 TTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGATT 3000

Qy   3001 TTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGA 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 TTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGA 3060

Qy   3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTCT 3120

Qy   3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 TAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGTC 3180

Qy   3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 CTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTCC 3240

Qy   3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGG 3300

Qy   3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCTG 3360

Qy   3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 CCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCAG 3420

Qy   3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480

Qy   3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540

Qy   3541 TTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 TTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600

Qy   3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660

Qy   3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 CAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
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RESULT 3

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PCT-US01-08631-9790
; Sequence 9790, Application PC/TUS0108631
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 21272-049
;  CURRENT APPLICATION NUMBER: PCT/US01/08631
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 9790
;   LENGTH: 3714
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (1419)..(2048)
;   OTHER INFORMATION: 98% homologous to Homo sapiens 68 kDa type I
;   OTHER INFORMATION: phosphatidylinositol-4-phosphate 5-kinase alpha,accession number
;   OTHER INFORMATION: U78575,Smith-Waterman Score=1078.
PCT-US01-08631-9790

  Query Match             99.7%;  Score 3702;  DB 1;  Length 3714;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3713;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 60

Qy       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120

Qy      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180

Qy      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240

Qy      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300

Qy      301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360

Qy      361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420

Qy      421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480

Qy      481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGCC 540

Qy      541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGAC 600

Qy      601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCT 660
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Qy      661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTT 720

Qy      721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAA 780

Qy      781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGA 840

Qy      841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGG 900

Qy      901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGA 960

Qy      961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 GGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCG 1020

Qy     1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCG 1080

Qy     1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCT 1140

Qy     1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 CAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCAC 1200

Qy     1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 ATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACAT 1260

Qy     1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGAT 1320

Qy     1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCTT 1380

Qy     1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAA-GGCTCTGT 1439
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     1381 AAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGGCTCTGT 1440

Qy     1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1500

Qy     1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1560

Qy     1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1620

Qy     1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1680

Qy     1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1740
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Qy    1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1800

Qy    1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1860

Qy    1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1920

Qy    1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1980

Qy    1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2040

Qy    2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2100

Qy    2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2160

Qy    2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2220

Qy    2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2280

Qy    2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2340

Qy    2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2400

Qy    2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2460

Qy    2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2520

Qy    2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2580

Qy    2580 TTTTTTTCTGAAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2639
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 TTTTTTTCTGAAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2640

Qy    2640 AACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGT 2699
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 AACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGT 2700

Qy    2700 TTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTC 2759
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 TTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTC 2760

Qy    2760 TCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTAT 2819
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 TCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTAT 2820

Qy    2820 CCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGAGATCATAGCCCTTCCTAGGCAGA 2879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 CCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGAGATCATAGCCCTTCCTAGGCAGA 2880

Qy    2880 ATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTGCAATTTGAAATATATTCTG 2939
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 ATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTGCAATTTGAAATATATTCTG 2940

Qy    2940 GTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGAT 2999
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 GTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGAT 3000

Qy    3000 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAG 3059
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAG 3060

Qy    3060 AGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTC 3119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 AGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTC 3120

Qy    3120 TTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGT 3179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 TTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGT 3180

Qy    3180 CCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTC 3239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 CCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTC 3240

Qy    3240 CCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGG 3299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 CCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGG 3300

Qy    3300 GGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCT 3359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 GGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCT 3360

Qy    3360 GCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCA 3419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 GCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCA 3420

Qy    3420 GTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTAT 3479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 GTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTAT 3480

Qy    3480 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCT 3539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCT 3540

Qy    3540 GTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAG 3599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 GTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAG 3600

Qy    3600 CAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAAT 3659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 CAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAAT 3660

Qy    3660 ACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 ACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3714


RESULT 4
US-09-770-175-8633
; Sequence 8633, Application US/09770175
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT:  Holtzman, Douglas A.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE: 1600.2058-001
;  CURRENT APPLICATION NUMBER: US/09/770,175
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 60/178,874
;  PRIOR FILING DATE: 2000-01-28
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;  NUMBER OF SEQ ID NOS: 8967
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8633
;   LENGTH: 4264
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-770-175-8633

  Query Match             99.4%;  Score 3690.8;  DB 30;  Length 4264;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3706;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 532

Qy         61 TGCCTCGTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 TGCCTCGTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 592

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 652

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 712

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        713 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 772

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 832

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 892

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 952

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 1012

Qy        540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 1072

Qy        600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 1132

Qy        660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 1192

Qy        720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 1252

Qy        780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 1312

Qy        840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 1372

Qy        900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 1432

Qy        960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1433 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1492

Qy       1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1493 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1552

Qy       1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1553 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1612

Qy       1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1613 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1672

Qy       1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1673 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1732

Qy       1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1733 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1792

Qy       1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1793 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1852

Qy       1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1853 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1912

Qy       1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1913 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1972

Qy       1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1973 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 2032

Qy       1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2033 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 2092

Qy       1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2093 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 2152

Qy       1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2153 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 2212

Qy       1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2213 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 2272

Qy       1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2273 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 2332

Qy       1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2333 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 2392

Qy       1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2393 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 2452

Qy       1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2280

Qy  2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
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Db  2281 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2340

Qy  2340 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TTGAATTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2400

Qy  2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2460

Qy  2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2520

Qy  2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2579
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2580

Qy  2580 TTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2639
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Db  2581 TTTTTTTCTGAAAAAAGGAAAA--CACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2638

Qy  2640 AACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGT 2699
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Db  2639 AACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGT 2698

Qy  2700 TTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTC 2759
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2699 TTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTC 2758

Qy  2760 TCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTAT 2819
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2759 TCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTAT 2818

Qy  2820 CCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGA 2879
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Db  2819 CCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGA 2878

Qy  2880 ATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTG 2939
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2879 ATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTG 2938

Qy  2940 GTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGAT 2999
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2939 GTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGAT 2998

Qy  3000 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAG 3059
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Db  2999 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAG 3058

Qy  3060 AGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTC 3119
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3059 AGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTC 3118

Qy  3120 TTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGT 3179
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3119 TTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGT 3178

Qy  3180 CCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTC 3239
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3179 CCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTC 3238

Qy  3240 CCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGG 3299
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3239 CCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGG 3298

Qy  3300 GGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCT 3359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3299 GGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCT 3358

Qy  3360 GCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCA 3419
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3359 GCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCA 3418

Qy  3420 GTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTAT 3479
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3419 GTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTAT 3478

Qy  3480 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCT 3539
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3479 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCT 3538

Qy  3540 GTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAG 3599
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3539 GTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAG 3598

Qy  3600 CAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAAT 3659
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3599 CAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAAT 3658

Qy  3660 ACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3659 ACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3712

RESULT 6
US-09-667-228-736
; Sequence 736, Application US/09667228
; GENERAL INFORMATION:
;  APPLICANT:  Gearing, David P.
;  APPLICANT:  Holtzman, Douglas A.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.1196-001
;  CURRENT APPLICATION NUMBER: US/09/667,228
;  CURRENT FILING DATE:  2000-09-21
;  PRIOR APPLICATION NUMBER:  60/154,931
;  PRIOR FILING DATE:  1999-09-21
;  NUMBER OF SEQ ID NOS:  756
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 736
;   LENGTH: 4266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-667-228-736

  Query Match             99.1%;  Score 3678.4;  DB 26;  Length 4266;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3712;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy     1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   473 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 532

Qy    61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   533 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 592

Qy   121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   593 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 652

Qy   181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   653 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 712

Qy   241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
         ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   713 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 772

Qy   300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 832

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 892

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 952

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 1012

Qy    540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 1072

Qy    600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 1132

Qy    660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 1192

Qy    720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 1252

Qy    780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 1312

Qy    840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 1372

Qy    900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 1432

Qy    960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1492

Qy   1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1493 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1552

Qy   1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1553 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1612

Qy   1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1613 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1672

Qy   1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1673 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1732

Qy   1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1733 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1792

Qy   1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   1793 TAATGGATTATAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1852

Qy   1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGT 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1853 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCAAAAGGCTCTGT 1912

Qy   1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1913 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1972

Qy   1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1973 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 2032

Qy   1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2033 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 2092

Qy   1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2093 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 2152

Qy   1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2153 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 2212

Qy   1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2213 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 2272

Qy   1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2273 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 2332

Qy   1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2333 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 2392

Qy   1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2393 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 2452

Qy   1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2453 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2512

Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2513 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2572

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2632

Qy   2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2692

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2752

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2812

Qy   2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2872

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2932

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2933 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2992
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Qy   2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   2993 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 3052

Qy   2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3053 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 3112

Qy   2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3113 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 3172

Qy   2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3173 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 3232

Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3233 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 3292

Qy   2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3293 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 3352

Qy   2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3353 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 3412

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3413 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 3472

Qy   2999 -TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3057
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3473 TTTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3532

Qy   3058 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3533 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3592

Qy   3118 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3593 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3652

Qy   3178 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3653 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3712

Qy   3238 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3713 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3772

Qy   3298 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3773 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3832

Qy   3358 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3833 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3892

Qy   3418 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3893 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3952

Qy   3478 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 3537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3953 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 4012

Qy   3538 CTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 3597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4013 CTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 4072

Qy   3598 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 3657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4073 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 4132

Qy   3658 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4133 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 4188


RESULT 7
US-09-699-997-11092
; Sequence 11092, Application US/09699997
; GENERAL INFORMATION:
;  APPLICANT:  Curtis, Rory A.J.
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  DiStefano, Peter
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2020-001
;  CURRENT APPLICATION NUMBER: US/09/699,997
;  CURRENT FILING DATE:  2000-10-30
;  PRIOR APPLICATION NUMBER:  60/162,359
;  PRIOR FILING DATE:  1999-10-29
;  NUMBER OF SEQ ID NOS:  12714
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 11092
;   LENGTH: 4266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-699-997-11092

  Query Match             99.1%;  Score 3678.4;  DB 27;  Length 4266;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3712;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    473 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 532

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 592

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 652

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 712

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    713 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 772

Qy    300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 832

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 892

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 952

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 1012

Qy    540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
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Db    1013 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 1072

Qy     600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 1132

Qy     660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 1192

Qy     720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
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Db    1193 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 1252

Qy     780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 1312

Qy     840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
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Db    1313 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 1372

Qy     900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1373 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 1432

Qy     960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1433 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1492

Qy    1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
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Db    1493 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1552

Qy    1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
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Db    1553 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1612

Qy    1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1613 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1672

Qy    1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1673 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1732

Qy    1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1733 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1792

Qy    1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1793 TAATGGATTATAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1852

Qy    1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
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Db    1853 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1912

Qy    1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
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Db    1913 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1972

Qy    1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1973 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 2032

Qy    1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
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Db    2033 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 2092

Qy    1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2093 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 2152

Qy    1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
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Db    2153 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 2212

Qy    1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
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Db    2213 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 2272

Qy    1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
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Db    2273 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 2332

Qy    1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
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Db    2333 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 2392

Qy    1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
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Db    2393 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 2452

Qy    1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
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Db    2453 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2512

Qy    2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2572

Qy    2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2632

Qy    2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
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Db    2633 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2692

Qy    2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2752

Qy    2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2753 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2812

Qy    2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2813 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2872

Qy    2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
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Db    2873 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2932

Qy    2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
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Db    2933 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2992

Qy    2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    2993 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 3052

Qy    2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3053 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 3112

Qy    2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
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Db    3113 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 3172

Qy    2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
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Db    3173 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 3232
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Qy   2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGACATGGGGTAATCTTTA 2818
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Db   3233 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGACATGGGGTAATCTTTA 3292

Qy   2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
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Db   3293 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 3352

Qy   2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
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Db   3353 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 3412

Qy   2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
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Db   3413 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 3472

Qy   2999 -TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3057
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Db   3473 TTTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3532

Qy   3058 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3117
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Db   3533 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3592

Qy   3118 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3593 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3652

Qy   3178 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3653 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3712

Qy   3238 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3713 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3772

Qy   3298 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3773 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3832

Qy   3358 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3833 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3892

Qy   3418 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCT 3477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3893 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTACAAGAAGGAAAGAATTCTTGCT 3952

Qy   3478 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 3537
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Db   3953 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 4012

Qy   3538 CTGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 3597
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Db   4013 CTGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 4072

Qy   3598 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 3657
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Db   4073 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 4132

Qy   3658 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
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Db   4133 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 4188

RESULT 8
US-09-726-802-2146
; Sequence 2146, Application US/09726802
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Falb, Dean A.
;  APPLICANT:  .
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2025-001
;  CURRENT APPLICATION NUMBER: US/09/726,802
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER:  60/168,012
;  PRIOR FILING DATE:  1999-11-30
;  NUMBER OF SEQ ID NOS:  2872
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2146
;   LENGTH: 4266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-726-802-2146

  Query Match             99.1%;  Score 3678.4;  DB 29;  Length 4266;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3712;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
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Db    473 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 532

Qy     61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 592

Qy    121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 652

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 712

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    713 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 772

Qy    300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 832

Qy    360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 892

Qy    420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 952

Qy    480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
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Qy    540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 1072

Qy    600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 1132

Qy    660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 1192

Qy    720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 1252

Qy    780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 1312
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Qy     840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 1372

Qy     900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1373 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 1432

Qy     960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1433 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1492

Qy    1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1493 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1552

Qy    1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1553 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1612

Qy    1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1613 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1672

Qy    1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1673 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1732

Qy    1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1733 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1792

Qy    1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1793 TAATGGATTATAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1852

Qy    1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1853 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1912

Qy    1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1913 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1972

Qy    1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1973 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 2032

Qy    1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2033 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 2092

Qy    1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2093 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 2152

Qy    1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2153 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 2212

Qy    1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2213 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 2272

Qy    1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 2332

Qy    1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2333 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 2392

Qy    1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 2452

Qy    1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2512

Qy    2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2572

Qy    2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2632

Qy    2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2692

Qy    2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2752

Qy    2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2753 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2812

Qy    2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2813 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2872

Qy    2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2873 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2932

Qy    2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2933 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2992

Qy    2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    2993 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 3052

Qy    2579 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3053 TTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 3112

Qy    2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3113 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 3172

Qy    2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3173 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 3232

Qy    2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3233 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 3292

Qy    2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3293 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 3352

Qy    2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3353 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 3412

Qy    2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3413 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 3472

Qy    2999 -TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3057
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Db       3473 TTTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3532

Qy       3058 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3533 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3592

Qy       3118 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3593 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3652

Qy       3178 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3653 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3712

Qy       3238 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3713 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3772

Qy       3298 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3832

Qy       3358 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3892

Qy       3418 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3952

Qy       3478 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 3537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3953 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 4012

Qy       3538 CTGTTAGGGGTGGAGGGAATATTTGAGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 3597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4013 CTGTTAGGGGTGGAGGGAATATTTGAGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 4072

Qy       3598 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 3657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4073 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 4132

Qy       3658 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4133 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 4188
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RESULT 9
US-09-726-809-2253
; Sequence 2253, Application US/09726809
; GENERAL INFORMATION:
;  APPLICANT:  Gearing, David P.
;  APPLICANT:  Holtzman, Douglas A.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2011-001
;  CURRENT APPLICATION NUMBER: US/09/726,809
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER:  60/168,039
;  PRIOR FILING DATE:  1999-11-30
;  NUMBER OF SEQ ID NOS:  3268
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 2253
;   LENGTH: 4266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-726-809-2253

  Query Match             99.1%;  Score 3678.4;  DB 29;  Length 4266;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3712;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;
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Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 532

Qy         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 652

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 712

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db        713 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 772

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 832

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 892

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 952

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 1012

Qy        540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 1072

Qy        600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 1132

Qy        660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 1192

Qy        720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 1252

Qy        780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 1312

Qy        840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 1372

Qy        900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1373 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 1432

Qy        960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1433 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1492

Qy       1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1493 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1552

Qy       1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1553 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1612

Qy    1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1613 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1672

Qy    1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1673 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1732

Qy    1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1733 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1792

Qy    1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
           |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1793 TAATGGATTATAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1852

Qy    1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1853 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1912

Qy    1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1913 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1972

Qy    1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1973 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 2032

Qy    1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2033 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 2092

Qy    1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2093 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 2152

Qy    1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2153 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 2212

Qy    1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2213 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 2272

Qy    1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2273 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 2332

Qy    1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2333 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 2392

Qy    1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2393 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 2452

Qy    1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2453 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2512

Qy    2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2513 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2572

Qy    2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2573 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2632

Qy    2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2633 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2692

Qy    2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2693 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2752

Qy    2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2753 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2812

Qy    2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2813 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2872

Qy    2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2873 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2932

Qy    2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2933 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2992

Qy    2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTC-TT 2578
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    2993 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 3052

Qy    2579 TTTTTTTTCTGAAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 2638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3053 TTTTTTTTCTGAAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCA 3112

Qy    2639 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 2698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3113 GAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTG 3172

Qy    2699 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 2758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3173 TTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCT 3232

Qy    2759 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 2818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3233 CTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTA 3292

Qy    2819 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 2878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3293 TCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAG 3352

Qy    2879 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 2938
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3353 AATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCT 3412

Qy    2939 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 2998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3413 GGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGA 3472

Qy    2999 -TTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3057
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3473 TTTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3532

Qy    3058 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3533 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3592

Qy    3118 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3593 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3652

Qy    3178 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3653 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3712

Qy    3238 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3713 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3772
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Qy       3298 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3773 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3832

Qy       3358 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3833 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3892

Qy       3418 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3893 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3952

Qy       3478 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 3537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3953 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 4012

Qy       3538 CTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 3597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4013 CTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 4072

Qy       3598 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 3657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4073 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 4132

Qy       3658 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4133 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 4188


RESULT 10
US-60-278-258-4040
; Sequence 4040, Application US/60278258
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION:  Polynucleotide Sequence Databases, and Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms Identified Thereby
;  FILE REFERENCE: GX-0010-1 P
;  CURRENT APPLICATION NUMBER: US/60/278,258
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 17730
;  SOFTWARE: PERL Program
; SEQ ID NO 4040
;   LENGTH: 3732
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 348086.4
US-60-278-258-4040

  Query Match            98.7%;  Score 3666.4;  DB 71;  Length 3732;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 3711;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    4;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 70

Qy         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 130

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 190

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 250

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        251 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 310

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 370

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 430

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 490

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCAT-GGCATCTGAGGTGCCTTATGCCTCTGGCATG 538
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        491 CCTCAGCATCTGGAATCAAGAGACCCATGGGCATCTGAGGTGCCTTATGCCTCTGGCATG 550

Qy        539 CCCAT-CAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAA 597
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 CCCATGCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAA 610

Qy        598 GACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAG 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 GACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAG 670

Qy        658 CCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTAT 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 CCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTAT 730

Qy        718 CTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTT 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        731 CTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTT 790

Qy        778 CAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGA 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        791 CAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGA 850

Qy        838 TGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAG 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        851 TGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAG 910

Qy        898 TGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAA 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        911 TGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAA 970

Qy        958 AGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCC 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        971 AGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCC 1030

Qy       1018 TCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACAT 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1031 TCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACAT 1090

Qy       1078 TCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGA 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1091 TCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGA 1150

Qy       1138 CCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCC 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1151 CCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCC 1210

Qy       1198 CACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGA 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1211 CACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGA 1270

Qy       1258 CATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAA 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1271 CATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAA 1330
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Qy   1318 GATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCC 1377
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   1331 GATAATGGATTATAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCC 1390

Qy   1378 CTTAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCT 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1391 CTTAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCT 1450

Qy   1438 GTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGAC 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1451 GTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGAC 1510

Qy   1498 TGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTA 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1511 TGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTA 1570

Qy   1558 TATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTG 1617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1571 TATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTG 1630

Qy   1618 GAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGA 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1631 GAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGA 1690

Qy   1678 ACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCC 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1691 ACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCC 1750

Qy   1738 TTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTC 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1751 TTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTC 1810

Qy   1798 CTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGC 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1811 CTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGC 1870

Qy   1858 AGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTT 1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1871 AGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTT 1930

Qy   1918 GGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGA 1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1931 GGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGA 1990

Qy   1978 GACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGA 2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1991 GACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGA 2050

Qy   2038 GTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGA 2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2051 GTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGA 2110

Qy   2098 TCCCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAA 2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2111 TCCCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAA 2170

Qy   2158 AAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTT 2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2171 AAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTT 2230

Qy   2218 CTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCA 2277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2231 CTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCA 2290

Qy   2278 TCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCAC 2337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2291 TCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCAC 2350

Qy   2338 TATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCA 2397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2351 TATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCA 2410

Qy   2398 GCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTA 2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2411 GCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTA 2470

Qy   2458 GCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTA 2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2471 GCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTA 2530

Qy   2518 ATCTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCT 2577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2531 ATCTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCT 2590

Qy   2578 TTTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATC 2637
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   2591 TTTTTTTTTCTGAAAAAAGG-AAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATC 2649

Qy   2638 AGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGT 2697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 AGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGT 2709

Qy   2698 GTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCC 2757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 GTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCC 2769

Qy   2758 TCTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTT 2817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 TCTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTT 2829

Qy   2818 ATCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCA 2877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 ATCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCA 2889

Qy   2878 GAATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTC 2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2890 GAATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTC 2949

Qy   2938 TGGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAG 2997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2950 TGGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAG 3009

Qy   2998 ATTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3010 ATTTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAA 3069

Qy   3058 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3070 AGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTT 3129

Qy   3118 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3130 TCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATAT 3189

Qy   3178 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3190 GTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCC 3249

Qy   3238 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3250 TCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAA 3309

Qy   3298 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3310 GGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACC 3369

Qy   3358 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3370 CTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGC 3429

Qy   3418 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3430 CAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCT 3489

Qy   3478 ATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 3537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     3490 ATTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTT 3549

Qy     3538 CTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 3597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3550 CTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGA 3609

Qy     3598 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 3657
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3610 AGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAA 3669

Qy     3658 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3670 ATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3725


RESULT 11
US-60-213-360-1871
; Sequence 1871, Application US/60213360
; GENERAL INFORMATION:
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION:  Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION:  Polynucleotide Sequence Databases, and Single Nucleotide Polymor
;  TITLE OF INVENTION:  Identified Thereby
;  FILE REFERENCE:  GX-0014 P
;  CURRENT APPLICATION NUMBER: US/60/213,360
;  CURRENT FILING DATE:  2000-06-21
;  NUMBER OF SEQ ID NOS:  8347
;  SOFTWARE:  PERL Program
; SEQ ID NO 1871
;   LENGTH: 3751
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 348086.4
US-60-213-360-1871

  Query Match             98.3%;  Score 3651.4;  DB 65;  Length 3751;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3710;  Conservative    0;  Mismatches    1;  Indels    8;  Gaps    5;

Qy        1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       27 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 86

Qy       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       87 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 146

Qy      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      147 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 206

Qy      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      207 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 266

Qy      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGAGGTGGCCCACAGA 299
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      267 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGAGGTGGCCCACAGA 326

Qy      300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      327 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 386

Qy      360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      387 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 446

Qy      420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      447 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 506

Qy      480 CCT---CAGCATCTGGAATCAAGAGACCCAT-GGCATCTGAGGTGCCTTATGCCTCTGGC 535
            |||   ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      507 CCTCAGCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGC 566

Qy      536 ATGCCCAT-CAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAA 594
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      567 ATGCCCATGCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAA 626

Qy      595 AAAGACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGG 654
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      627 AAAGACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGG 686

Qy      655 GAGCCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAG 714
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      687 GAGCCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAG 746

Qy      715 TATCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCG 774
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      747 TATCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCG 806

Qy      775 TTTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCC 834
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      807 TTTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCC 866

Qy      835 CGATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGC 894
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      867 CGATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGC 926

Qy      895 TAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACA 954
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      927 TAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACA 986

Qy      955 TAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAA 1014
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      987 TAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAA 1046

Qy     1015 CCCTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAA 1074
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1047 CCCTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAA 1106

Qy     1075 CATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATA 1134
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1107 CATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATA 1166

Qy     1135 TGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCT 1194
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1167 TGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCT 1226

Qy     1195 TCCCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGC 1254
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1227 TCCCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGC 1286

Qy     1255 TGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTT 1314
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1287 TGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTT 1346

Qy     1315 CAAGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGA 1374
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1347 CAAGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGA 1406

Qy     1375 GCCCTTAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGC 1434
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1407 GCCCTTAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGC 1466

Qy     1435 TCTGTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGA 1494
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1467 TCTGTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGA 1526

Qy     1495 GACTGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCT 1554
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1527 GACTGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCT 1586
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Qy   1555 TTATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTC 1614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1587 TTATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTC 1646

Qy   1615 TTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGC 1674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1647 TTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGC 1706

Qy   1675 TGAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTC 1734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1707 TGAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTC 1766

Qy   1735 TCCTTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAA 1794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1767 TCCTTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAA 1826

Qy   1795 CTCCTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAA 1854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1827 CTCCTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAA 1886

Qy   1855 GGCAGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACC 1914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1887 GGCAGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACC 1946

Qy   1915 TTTGGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGG 1974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1947 TTTGGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGG 2006

Qy   1975 AGAGACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTC 2034
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   2007 AGAGACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAGAGCTTGAAGTTGCAGAGTC 2066

Qy   2035 AGAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTG 2094
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2067 AGAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTG 2126

Qy   2095 TGATCCCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCA 2154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2127 TGATCCCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCA 2186

Qy   2155 AAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAAC 2214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2187 AAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAAC 2246

Qy   2215 CTTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCA 2274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2247 CTTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCA 2306

Qy   2275 GCATCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTC 2334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2307 GCATCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTC 2366

Qy   2335 CACTATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTG 2394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367 CACTATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTG 2426

Qy   2395 GCAGCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGA 2454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2427 GCAGCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGA 2486

Qy   2455 CTAGCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCT 2514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2487 CTAGCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCT 2546

Qy   2515 GTAATCTCTGTAAAGGTTTTTGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCT 2574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2547 GTAATCTCTGTAAAGGTTTTTGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCT 2606

Qy   2575 TCTTTTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAG 2634
          |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db   2607 TCTTTTTTTTTTCTGAAAAAAGGAAAA--CACACAGCACACAATTTCAAGCCATTTTCAG 2664

Qy   2635 ATCAGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCAT 2694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2665 ATCAGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCAT 2724

Qy   2695 GGTGTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCC 2754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2725 GGTGTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCC 2784

Qy   2755 TCCTCTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATC 2814
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2785 TCCTCTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATC 2844

Qy   2815 TTTATCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAG 2874
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2845 TTTATCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAG 2904

Qy   2875 GCAGAATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATA 2934
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2905 GCAGAATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATA 2964

Qy   2935 TTCTGGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAG 2994
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2965 TTCTGGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAG 3024

Qy   2995 GAGATTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGG 3054
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3025 GAGATTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGG 3084

Qy   3055 TAAAGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATA 3114
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3085 TAAAGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATA 3144

Qy   3115 TTTTCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCA 3174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3145 TTTTCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCA 3204

Qy   3175 TATGTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTC 3234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3205 TATGTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTC 3264

Qy   3235 TCCTCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAA 3294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3265 TCCTCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAA 3324

Qy   3295 GAAGGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCC 3354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3325 GAAGGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCC 3384

Qy   3355 ACCCTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCC 3414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3385 ACCCTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCC 3444

Qy   3415 AGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTT 3474
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3445 AGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTT 3504

Qy   3475 GCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGA 3534
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Db   3505 GCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGA 3564

Qy   3535 GTTCTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGG 3594
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Db   3565 GTTCTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGG 3624

Qy   3595 GGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGG 3654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3625 GGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGG 3684

Qy   3655 CAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3685 CAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3743
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RESULT 12
US-60-172-373-4035
; Sequence 4035, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 4035
;   LENGTH: 3787
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 348086.4
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 3766, 3771, 3774-3775, 3779, 3783
;   OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-4035

  Query Match             96.9%;  Score 3599.2;  DB 61;  Length 3787;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 3705;  Conservative    0;  Mismatches    8;  Indels   11;  Gaps    9;

Qy          1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         37 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGACTTTTCA 96

Qy         61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 156

Qy        121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 216

Qy        181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 276

Qy        241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        277 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 336

Qy        300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 396

Qy        360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 456

Qy        420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 516

Qy        480 CCTCAGCATCTGGAATCAAGAGACCCAT-GGCATCTGAGGTGCCTTATGCCTCTGGCATG 538
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        517 CCTCAGCATCTGGAATCAAGAGACCCATGGGCATCTGAGGTGCCTTATGCCTCTGGCATG 576

Qy        539 CCCAT-CAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAA 597
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 CCCATGCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAA 636

Qy        598 GACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAG 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 GACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAG 696

Qy        658 CCTGAGTACCAAACCAGAGCGTGATGTCCTCATG-CAAGATTTCTACGTGGTTGAGAGTA 716
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        697 CCTGAGTACCAAACCAGAGCGTGATGTCCTCATGTCAAGATTTCTACGTGGTTGAGAGTA 756

Qy        717 TCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTT 776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        757 TCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTT 816

Qy        777 TCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCG 836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 TCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCG 876

Qy        837 ATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTA 896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        877 ATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTA 936

Qy        897 GTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATA 956
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        937 GTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATA 996

Qy        957 AAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACC 1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        997 AAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACC 1056

Qy       1017 CTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACA 1076
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1057 CTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACA 1116

Qy       1077 TTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATG 1136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1117 TTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATG 1176

Qy       1137 ACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTC 1196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1177 ACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTC 1236

Qy       1197 CCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTG 1256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1237 CCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTG 1296

Qy       1257 ACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCA 1316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1297 ACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCA 1356

Qy       1317 AGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCAT-GCACAACGAGAG 1375
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1357 AGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGGCACAACGAGAG 1416

Qy       1376 CCCTTAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCT 1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1417 CCCTTAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCT 1476

Qy       1436 CTGTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAG 1495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1477 CTGTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAG 1536

Qy       1496 ACTGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTT 1555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1537 ACTGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTT 1596

Qy       1556 TATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCT 1615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1597 TATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCT 1656

Qy       1616 TGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCT 1675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1657 TGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCT 1716

Qy       1676 GAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCT 1735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1717 GAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCT 1776
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Qy   1736 CCTTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAAC 1795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 CCTTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAAC 1836

Qy   1796 TCCTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAG 1855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1837 TCCTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAG 1896

Qy   1856 GCAGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCT 1915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 GCAGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCT 1956

Qy   1916 TTGGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGA 1975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 TTGGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGA 2016

Qy   1976 GAGACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCA 2035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 GAGACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCA 2076

Qy   2036 GAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGT 2095
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Db   2077 GAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGT 2136

Qy   2096 GATCCCAAGATGT-CAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCA 2154
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 GATCCCAAGATGTCCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCA 2196

Qy   2155 AAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAAC 2214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 AAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAAC 2256

Qy   2215 CTTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCA 2274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 CTTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCA 2316

Qy   2275 GCATCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTC 2334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 GCATCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTC 2376

Qy   2335 CACTATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTG 2394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2377 CACTATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTG 2436

Qy   2395 GCAGCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGA 2454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2437 GCAGCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGA 2496

Qy   2455 CTAGCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCT 2514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2497 CTAGCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCT 2556

Qy   2515 GTAATCTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTT---CT 2571
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2557 GTAATCTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTTCCTC 2616

Qy   2572 TCTTCTTTTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAA-TTTCAAGCCATTT 2630
               |||||||||||||||||||||||||| |||||||||||||| |||||||||||||
Db   2617 CTCCTTTTTTTTTTTCTGAAAAAAGGAAAAACCACACAGCACACAATTTTCAAGCCATTT 2676

Qy   2631 TCAGATCAGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAG 2690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2677 TCAGATCAGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAG 2736

Qy   2691 CCATGGTGTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAA 2750
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Db   2737 CCATGGTGTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAA 2796

Qy   2751 CTCCTCCTCTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGACATGGGGT 2810
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2797 CTCCTCCTCTCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGACATGGGGT 2856

Qy   2811 AATCTTTATCCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTC 2870
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Qy   2871 CTAGGCAGAATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAA 2930
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Db   2917 CTAGGCAGAATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAA 2976

Qy   2931 TATATTCTGGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCC 2990
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Qy   2991 AGAGGAGATTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCT 3050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3037 AGAGGAGATTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCT 3096

Qy   3051 AAGGTAAAGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGG-CCAGC 3109
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   3097 AAGGTAAAGAGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCCAGC 3156

Qy   3110 AAATATTTTCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTG 3169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3157 AAATATTTTCTTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTG 3216

Qy   3170 TGCCATATGTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATG 3229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3217 TGCCATATGTCCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATG 3276

Qy   3230 CCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAG 3289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3277 CCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAG 3336

Qy   3290 GGGAAGAAGGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCT 3349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3337 GGGAAGAAGGGGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCT 3396

Qy   3350 ATCCCACCCTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACA 3409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3397 ATCCCACCCTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACA 3456

Qy   3410 CCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAA 3469
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Db   3457 CCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAA 3516

Qy   3470 TTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGG 3529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3517 TTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGG 3576

Qy   3530 ACAGAGTTCTGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGG 3589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3577 ACAGAGTTCTGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGG 3636

Qy   3590 AATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGA 3649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3637 AATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGA 3696

Qy   3650 AATGGCAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTA 3709
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3697 AATGGCAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTA 3756

Qy   3710 TTTA 3713
          ||||
Db   3757 TTTA 3760
```

```
RESULT 13
US-60-212-356-49/c
; Sequence 49, Application US/60212356
; GENERAL INFORMATION:
;  APPLICANT:  Beasley, Ellen
;  TITLE OF INVENTION:  ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
```

```
;  FILE REFERENCE:  CL000677
;  CURRENT APPLICATION NUMBER: US/60/212,356
;  CURRENT FILING DATE:  2000-06-19
;  NUMBER OF SEQ ID NOS:  411
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 32768
;   TYPE: DNA
;   ORGANISM: HUMAN
US-60-212-356-49

  Query Match             81.8%;  Score 3038.4;  DB 65;  Length 32768;
  Best Local Similarity   91.2%;  Pred. No. 0;
  Matches 3420;  Conservative    0;  Mismatches  276;  Indels   56;  Gaps   16;

Qy        2 TTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCAT 61
            | |||||||||||| |||| ||||| |||| | ||||||||||||| ||||||||||||
Db    12171 TAAACAGGCCGTGGGTAGGGAGGACAGAGAGGCGGCGTTCGCTCCTCTGGGACTTTTCAC 12112

Qy       62 GCCTCG-------TTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCC 114
            ||||||       |||||| ||||||||||||||  ||  | |||| ||||| ||||| |
Db    12111 GCCTCGTTTTGTTTTTTTTTCTTCAGATGTGGCTTTTTCCTGACGCAGGGTCCAAGCAGTC 12052

Qy      115 AGCTTAAGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTT 174
            ||||| |||||||||||||||||||| ||||||| ||| ||| ||||||||||| |||||
Db    12051 AGCTTGAGCTTACTCTTCTGTGAAAGCGGAAAGTCTCCTCTGAGGAAAGCGGTTGAACTT 11992

Qy      175 GTGGAGGGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGC 234
            |||||||| ||||| |||| | ||||| ||||||||||||||||||||| ||||||||||
Db    11991 GTGGAGGGCGTGCGAGACGGGCGTTCTCCCCCATGCCAGGCGAATGGTGCGGCCTTGAGC 11932

Qy      235 TGGTCCAGGAGCCGGCTC---GACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTG 290
            |||||||| |||||||||   |||  |||||||||||| ||| |||| |||||| |||||
Db    11931 TGGTCCAGCAGCCGGCTCGATGACAGGTCTGAGGGAGGCCCCAGAGGCGGCGGGAAGGTG 11872

Qy      291 GCCCACAGAACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAA 350
            |||| |||||||||||||||||||||| |||| | ||||||||||||||||||| |||||
Db    11871 GCCCGCAGAACGCGGGTTCTGTAAAGACACGTGGAGAAGATTCGATTCCGAGAACAGGAA 11812

Qy      351 GAACCGGATTGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGG 410
            ||  ||||| |||||| |||||||| ||||  ||| |||||||||| |||||||||||||
Db    11811 GAGGCGGATGGAAAGACAGCCAGGCGGCTGCCGGGAAGGGGGCTGCCAAGATGGCGTCGG 11752

Qy      411 CCTCCTCCGGGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCT 470
            ||||||||   |||||||   ||||||||||||||||||||||||||| || ||||||||
Db    11751 CCTCCTCCCAACCGTCGTTGGCGGTCGGTTTTTCATCCTTTGATCCCGGGGCCCCTTCCT 11692

Qy      471 GTACCTTGTCCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCT 530
            |||||  |||||||||||||||||||  ||| |||| |||||||||||||||||||||||
Db    11691 GTACCGCGTCCTCAGCATCTGGAATCTTGAGCCCCACGGCATCTGAGGTGCCTTATGCCT 11632

Qy      531 CTGGCATGCCCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACAT 590
            ||||||||||||||||||||| ||||||| || |||| ||||||||||||||||||||||
Db    11631 CTGGCATGCCCATCAAGAAAACAGGCCATCGAGGTGTCGATTCCTCAGGAGAGACAACAT 11572

Qy      591 ATAAAAAGACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTG 650
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||  ||||||
Db    11571 ATAAAAAGACAACCTCAACAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACTTACACTG 11512

Qy      651 TGGGGAGCCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTG 710
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    11511 TGGGGAGCCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTGG 11452

Qy      711 AGAGTATCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACT 770
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| ||
Db    11451 AGAGTATCTTCTTCCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGCCT 11392

Qy      771 TTCGTTTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCC 830
            | ||||||||||||||||| || ||||||||||||||||| |||||||||||||||||||
Db    11391 TCCGTTTCAAGACCTATGCGCCGGTTGCCTTCCGCTACTTTCGGGAGCTATTTGGTATCC 11332

Qy      831 GGCCCGATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTG 890
             |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db    11331 CGCCCGATGATTACTTGTGCTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTG 11272

Qy      891 GAGCTAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCC 950
            |||||||||||||||| |||||||||||||||||||||||  |||||||||||||| |||
Db    11271 GAGCTAGTGGTTCCCTGTTCTATGTGTCCAGCGACGATGAACTCATTATTAAGACACTCC 11212

Qy      951 AACATAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACC 1010
            |||||||||||||||| |||||||||||||||||||||||||||||| ||||||||| ||
Db    11211 AACATAAAGAGGCGGAGTTTCTGCAGAAGCTGCTTCCAGGATACTACTTGAACCTCAGCC 11152

Qy     1011 AGAACCCTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCA 1070
            |||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db    11151 AGAACCCTCGGACTTTGCTGCCTAAATTCTTTGGACTGTACTGTGTGCAGACAGGTGGCA 11092

Qy     1071 AGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCA 1130
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Db    11091 AGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCCGTCAAAATGCATATCA 11032

Qy     1131 AATATGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGC 1190
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    11031 AATATGACCTCAAAGGCTCAACCTACAAACGCCGGGCTTCCCAGAAAGAGCGAGAGAAGC 10972

Qy     1191 CTCTTCCCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGG 1250
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    10971 CTCTTCCCACATTTAAAGATCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGG 10912

Qy     1251 ATGCTGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGA 1310
            ||||||||| |||||| |||||||||||||||||||||||||||||||||||||||||||
Db    10911 ATGCTGACACGTACAATGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGA 10852

Qy     1311 GCTTCAAGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAAC 1370
            |||||||||||||||| || ||||||| | |||||||||| |||||||||||||||||||
Db    10851 GCTTCAAGATAATGGACTATAGCCTCTGGCTGTCAATCCACAATATAGATCATGCACAAC 10792

Qy     1371 GAGAGCCCTTAAGCAGTGAAACACAGTA---CTCAGTTGATACTCGAAGACCGGCCCCCC 1427
            |||||||||||||||| || || |   |    ||| | || |||| ||||| ||| ||||
Db    10791 GAGAGCCCTTAAGCAGCGACACTCTTCAAGTGTCAATCGACACTCAAAGACTGGCTCCCC 10732

Qy     1428 AAAAGGCTCTGTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTA 1487
            |||||||||||||||||||||||||||||| |||||||||||||||||| | ||| |  |
Db    10731 AAAAGGCTCTGTATTCCACAGCCATGGAATTCATCCAGGGAGAGGCTCGGCTGGGCGACA 10672

Qy     1488 CCATGGAGACTGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGC 1547
            |||||||| | |||||||||||||||||||||||||| | ||||||||||||||||||||
Db    10671 CCATGGAGGCCGATGACCATATGGGTGGCATCCCTGCTCAGAATAGTAAAGGGGAAAGGC 10612

Qy     1548 TTCTGCTTTATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGG 1607
            |||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||
Db    10611 TTCTGCTTTATATTGGCATCATTGACATTCTACAGTCTTACACGTTTCTTAAGAAGTTGG 10552

Qy     1608 AGCACTCTTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCT 1667
            ||||||||||||||||| |||||||||| || ||| ||||||||||||||||||||||||
Db    10551 AGCACTCTTGGAAAGCCGTGGTACATGATGGGGACGCTGTCTCAGTGCATCGCCCAGGCT 10492

Qy     1668 TCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGA 1727
            ||||||||||||||||||||| ||||||||||||| |||||||||||||||| |||||||
Db    10491 TCTACGCTGAACGGTTCCAGCACTTCATGTGCAACGCAGTATTTAAGAAGATCCCCTTGA 10432

Qy     1728 AGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCA 1787
            ||||||||||||||||||||||||||||||||| ||||||||||| ||   | |||||||
Db    10431 AGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTTATCTTTCTCTCTGCATACGGGCTCCA 10372

Qy     1788 GTGGCAACTCCTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGA 1847
            |||||||||||||||||||||||||||||| |||||||| |||||||||| ||||||||
Db    10371 GTGGCAACTCCTGCATTACTTACCAGCCATTGGTCTCTGAGGAACACAAGTCACAAGTG- 10313

Qy     1848 CAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGA 1907
              | |||||   ||||||||||||| ||||||||||||||| ||||||||||||||||||
Db    10312 --ATAAAGGTGCAAGTGGAGCCAGGTGTTCACCTTGGTCGTTCTGATGTTTTACCTCAGA 10255

Qy     1908 C-------TCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTC 1960
            |       ||||||||||||||||||||||||||||||  ||||| |||||| |||||||
Db    10254 CCTCAGAATCCACCTTTGGAGGAAATCAGTGAGGGCTC-ACTATTACTGACCACAGTTTC 10196
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Qy       1961 TCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTT 2020
              |||||| |||||||| |||||||||| |||||||||||||||| |||||||||||| |||
Db      10195 TCACCTGTAGTTGGAAAGACTTTGCATATGCTAACTACAAGTATAACCTTGGAAAAACTT 10136

Qy       2021 GAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGA 2080
              |||  | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10135 GAATGTACAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGA 10076

Qy       2081 TTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTT 2140
              ||||| | |||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      10075 TTCTG-CTTCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAGCAATGTTGAATTTTCTT 10017

Qy       2141 CTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCT 2200
              |||||||||||||||||||||||||||| ||||| |||| |  ||    |||||||||||
Db      10016 CTACTTGGTCATCAAAAAAGGAGTGTAAAAGAAGCGAGGTGCACT----CTCCATCTTCT 9961

Qy       2201 TCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAG 2260
              |||||||||||| ||| || | ||||    ||||||| ||||||| |||||||||  ||
Db       9960 TCCTGAAGAAGAGCCTCCTATTCTTCTCTGTCCTCATAAATGGGCATTAGTGCCTTGGAC 9901

Qy       2261 AGTTGAGGA--------------CCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGTACG 2306
              |||||||||              || |||||||||||||||||||||||||||||| |||
Db       9900 AGTTGAGGACCACTCCATCCTCTCCACAGCATCCCCTCCACTCCAGAGTTGGGTGGCACG 9841

Qy       2307 GATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATTCTT 2366
              |||||||||||||| || |||| || ||||| | ||||||||||||||||||||||||||
Db       9840 GATTTTCAACTGGCTAA-CCTTGGCTTCCACAACTGAATTTTTTTCAGACCCCCATTCTT 9782

Qy       2367 CATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTAGGA 2426
              ||||||||||||| || | ||||||||||||| ||||||||||||| ||||| || ||||
Db       9781 CATGCTGGAAATGAGACTACTGGACTTGGCAGTTTTCTTTCCCCTCATCTTTCACCAGGA 9722

Qy       2427 ACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTTCTT 2486
              || |||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Db       9721 ACTGGACTCTTAATTTCCTCAGGACAGACTAGCTGCCACATTATCCCCACCTTAGTTCTT 9662

Qy       2487 TCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATAAGG 2546
              |||||||||  |||||||||| || ||||||||||||||| |||||||||||||||||||
Db       9661 TCTCTCTGATCCCTGGAAGAAAACCCCTGTAATCTCTGTATAGGTTTTTGGGGGATAAGG 9602

Qy       2547 GTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTTTTTTTTCTGAAAAAAGGAAAAAGCAC 2606
              |||||||||||||||||| ||   || || ||||||||| |||||||||||||||||| |
Db       9601 GTGTTTAACCACCTCCCAACT---TTGTTTTTTTTTTTTCCTGAAAAAAGGAAAAAGCGC 9545

Qy       2607 ACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGATGCCT 2666
              |||||||  |||||||||||| |||||||||| || ||||||||||||||| ||||||||
Db       9544 ACAGCACCAAATTTCAAGCCAGTTTCAGATCAAAAATCCAGAAGTGTTGACGAGATGCCT 9485

Qy       2667 ATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATTGCTC 2726
              || ||||| |||||||||||||||||| ||||||| ||||| ||| ||||||||||||||
Db       9484 ATCCGTAGGGTTCCCTCAGAAGAGCCACGGTGTTTGTGAAGGGAAAAGTAGTGATTGCTC 9425

Qy       2727 TGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTGAAGG 2786
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db       9424 TGCCAGAAGCAGCTCCTCTTTAAACTCCTCATCTCTTGATGAATTTCTTAAGGCTGAAGG 9365

Qy       2787 AATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCAGCCA 2846
              |||| |||||||||||| |||||||||||||| | |||||||||||||| ||||||||||
Db       9364 AATGGAGAGAGTGGGACGTGGGGTAATCTTTACCACTTTTGTTAAAACATGAGGCAGCCA 9305

Qy       2847 TGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATAGTAA 2906
              |||| ||||||||||||||||||||| ||||||||||| ||||||||||||||||| | |
Db       9304 TGGGTTGGGAGATCATAGCCCTTCCTGGGCAGAATCCTATTCACTGCCAGGCTATAATGA 9245

Qy       2907 TTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGACTTAC 2966
              |||||||| |||||||||||||||||||||||||||| |||||||||| |||||||||||
Db       9244 TTATTACTGTTTTGCAATTTGAAATATATTCTGGTTGCTTTTCTAAATATGAAGACTTAC 9185

Qy       2967 CAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTTCCAA 3026
              ||||||||||||||||||||||||| |||||| |||||||||||||| ||||||||||||
Db       9184 CAAATGAATTTTAGATCATTCTCCAAAGGAGA-TTTTTTTGCTCTTCCCATCTTTTCCAA 9126

Qy       3027 CAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAACAGA 3086
              |||||||||||||||||||| |||||||| |||||||||||| ||||||||||||||||
Db       9125 CAGTGTTCTCCTGTTTGTGGTGCTAAGGTGAAGAGGGGACACCTCTGTCTGTTTAACAGG 9066

Qy       3087 CAGTCCATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAGATTC 3146
              |||||| ||||||||||||||||||||||||||||||| ||||||||||||||  |||||
Db       9065 CAGTCCGTATCTGTGAGGCCAGCAAATATTTTCTTAAATTCATGGGGAGACAGTGGATTC 9006

Qy       3147 TTGCCTTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCCCTGTCTTCATGCAGGGAA 3206
              |||||| ||||||||||||||| |||||||||||||||||||  |||||||||||| |||
Db       9005 TTGCCTCGGTGAGGTCATTGCTATGCCATATGTCCTACCCCC--GTCTTCATGCAGAGAA 8948

Qy       3207 GTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTTTCCA 3266
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db       8947 GTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCACCTACAAGAGTTGTGGTTTTCCA 8888

Qy       3267 TCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGGGGCCTGGTATCTCAGGCAGATTGTTG 3326
              ||||||||||||||| |||||||| ||||||||||||||||||||||||||| |||||||
Db       8887 TCTGATCCTTCCACTGTTGTCAGGAGAAGAAGGGGGCCTGGTATCTCAGGCATATTGTTG 8828

Qy       3327 AATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGATAATATGTTAGCCCATACCC 3386
              |||||||||||||||||||||||||||||||||||||||| | || ||||||||||||||
Db       8827 AATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGACAGTAGGTTAGCCCATACCC 8768

Qy       3387 CAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCA 3446
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8767 CAAATAACTTTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCA 8708

Qy       3447 TG---TTTTTTACAAGAAGGAAAGAATTCTTGCT--ATTTTTTTTTCATAATTTACTATT 3501
              ||   |||||||||||||||||||||    | ||   | |||||||||||||||||||||
Db       8707 TGTTCTTTTTTACAAGAAGGAAAGAAACAATTCTTGCTATTTTTTTCATAATTTACTATT 8648

Qy       3502 TATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATT 3561
              |||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||
Db       8647 TATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTAAGGGGTGGAGAGAATATT 8588

Qy       3562 TGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTAC 3621
              ||||||||||||||||||||||||||||||| ||||| ||||||||| || ||||||  |
Db       8587 TGAGGGAGGGCTGGGTCTTAGGGAAAGGAATAGGGAATCAACATTTTAATGAAGTGTCTC 8528

Qy       3622 TATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGG 3681
              ||||||| ||||||||||||  ||| |||| ||||||| |||||||||||||||||||||
Db       8527 TATTTGCTTCTACTTTGTATCATTCGGAAAAGGCAAATGCAATATAAAAGTGATATATGG 8468

Qy       3682 TTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
              ||||||||||||||||||| || |||||||||
Db       8467 TTTTAATGTAATAAACTTTTATCAGTTATTTA 8436
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RESULT 14
US-60-229-525-42/c
; Sequence 42, Application US/60229525
; GENERAL INFORMATION:
;  APPLICANT:  Beasley, Ellen
;  TITLE OF INVENTION:  ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
;  TITLE OF INVENTION:  NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
;  TITLE OF INVENTION:  PROTEINS, AND USES THEREOF
;  FILE REFERENCE:  CL000772
;  CURRENT APPLICATION NUMBER: US/60/229,525
;  CURRENT FILING DATE:  2000-09-05
;  NUMBER OF SEQ ID NOS:  819
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 32768
;   TYPE: DNA
;   ORGANISM: HUMAN
US-60-229-525-42

  Query Match             81.8%;  Score 3038.4;  DB 66;  Length 32768;
  Best Local Similarity   91.2%;  Pred. No. 0;
  Matches 3420;  Conservative    0;  Mismatches  276;  Indels   56;  Gaps   16;

Qy          2 TTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCAT 61
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          | |||||||||||| |||| ||||| |||| | ||||||||||||| ||||||||||||
Db  12172 TAAACAGGCCGTGGGTAGGGAGGACAGAGAGGCGGCGTTCGCTCCTCTGGGACTTTTCAC 12113

Qy     62 GCCTCG-------TTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCC 114
          ||||||       |||||| ||||||||||||||  ||  | |||| ||||| ||||| |
Db  12112 GCCTCGTTTTGTTTTTTTTCTTCAGATGTGGCTTTTTCCTGACGCAGGGTCCAAGCAGTC 12053

Qy    115 AGCTTAAGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTT 174
          ||||| |||||||||||||||||||| ||||||| ||| ||| ||||||||||| |||||
Db  12052 AGCTTGAGCTTACTCTTCTGTGAAAGCGGAAAGTCTCCTCTGAGGAAAGCGGTTGAACTT 11993

Qy    175 GTGGAGGGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGC 234
          |||||||| ||||| |||| | ||||| ||||||||||||||||||||| ||||||||||
Db  11992 GTGGAGGGCGTGCGAGACGGGCGTTCTCCCCCATGCCAGGCGAATGGTGCGGCCTTGAGC 11933

Qy    235 TGGTCCAGGAGCCGGCTC---GACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTG 290
          |||||||| |||||||||   |||  |||||||||||| ||| |||| |||||| |||||
Db  11932 TGGTCCAGCAGCCGGCTCGATGACAGGTCTGAGGGAGGCCCCAGAGGCGGCGGGAAGGTG 11873

Qy    291 GCCCACAGAACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAA 350
          |||| |||||||||||||||||||||| |||| | ||||||||||||||||||| |||||
Db  11872 GCCCGCAGAACGCGGGTTCTGTAAAGACACGTGGAGAAGATTCGATTCCGAGAACAGGAA 11813

Qy    351 GAACCGGATTGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGG 410
          ||  ||||| |||||| |||||||| ||||  ||| |||||||||| |||||||||||||
Db  11812 GAGGCGGATGGAAAGACAGCCAGGCGGCTGCCGGGAAGGGGGCTGCCAAGATGGCGTCGG 11753

Qy    411 CCTCCTCCGGGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCT 470
          ||||||||   |||||||   ||||||||||||||||||||||||||| || ||||||||
Db  11752 CCTCCTCCCAACCGTCGTTGGCGGTCGGTTTTTCATCCTTTGATCCCGGGGCCCCTTCCT 11693

Qy    471 GTACCTTGTCCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCT 530
          |||||  |||||||||||||||||||  ||| |||| |||||||||||||||||||||||
Db  11692 GTACCGCGTCCTCAGCATCTGGAATCTTGAGCCCCACGGCATCTGAGGTGCCTTATGCCT 11633

Qy    531 CTGGCATGCCCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACAT 590
          ||||||||||||||||||||| ||||||| || |||| ||||||||||||||||||||||
Db  11632 CTGGCATGCCCATCAAGAAAACAGGCCATCGAGGTGTCGATTCCTCAGGAGAGACAACAT 11573

Qy    591 ATAAAAAGACAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTG 650
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||  ||||||
Db  11572 ATAAAAAGACAACCTCAACAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACTTACACTG 11513

Qy    651 TGGGGAGCCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTG 710
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  11512 TGGGGAGCCTGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTGG 11453

Qy    711 AGAGTATCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACT 770
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| ||
Db  11452 AGAGTATCTTCTTCCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGCCT 11393

Qy    771 TTCGTTTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCC 830
          | ||||||||||||||||| || ||||||||||||||||| |||||||||||||||||||
Db  11392 TCCGTTTCAAGACCTATGCGCCGGTTGCCTTCCGCTACTTTCGGGAGCTATTTGGTATCC 11333

Qy    831 GGCCCGATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTG 890
           |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db  11332 CGCCCGATGATTACTTGTGCTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTG 11273

Qy    891 GAGCTAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCC 950
          |||||||||||||||| |||||||||||||||||||||||  |||||||||||||| |||
Db  11272 GAGCTAGTGGTTCCCTGTTCTATGTGTCCAGCGACGATGAACTCATTATTAAGACACTCC 11213

Qy    951 AACATAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACC 1010
          |||||||||||||||| |||||||||||||||||||||||||||||| ||||||||| ||
Db  11212 AACATAAAGAGGCGGAGTTTCTGCAGAAGCTGCTTCCAGGATACTACTTGAACCTCAGCC 11153

Qy   1011 AGAACCCTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCA 1070
          |||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db  11152 AGAACCCTCGGACTTTGCTGCCTAAATTCTTTGGACTGTACTGTGTGCAGACAGGTGGCA 11093

Qy   1071 AGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCA 1130
          ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Db  11092 AGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCCGTCAAAATGCATATCA 11033

Qy   1131 AATATGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGC 1190
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  11032 AATATGACCTCAAAGGCTCAACCTACAAACGCCGGGCTTCCCAGAAAGAGCGAGAGAAGC 10973

Qy   1191 CTCTTCCCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGG 1250
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  10972 CTCTTCCCACATTTAAAGATCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGG 10913

Qy   1251 ATGCTGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGA 1310
          ||||||||| |||||| |||||||||||||||||||||||||||||||||||||||||||
Db  10912 ATGCTGACACGTACAATGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGA 10853

Qy   1311 GCTTCAAGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAAC 1370
          |||||||||||||||| || ||||||| | |||||||||| |||||||||||||||||||
Db  10852 GCTTCAAGATAATGGACTATAGCCTCTGGCTGTCAATCCACAATATAGATCATGCACAAC 10793

Qy   1371 GAGAGCCCTTAAGCAGTGAAACACAGTA---CTCAGTTGATACTCGAAGACCGGCCCCCC 1427
          |||||||||||||||| || || |   |    ||| | || |||| ||||| ||| ||||
Db  10792 GAGAGCCCTTAAGCAGCGACACTCTTCAAGTGTCAATCGACACTCAAAGACTGGCTCCCC 10733

Qy   1428 AAAAGGCTCTGTATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTA 1487
          |||||||||||||||||||||||||||||| |||||||||||||||||| | ||| |  |
Db  10732 AAAAGGCTCTGTATTCCACAGCCATGGAATTCATCCAGGGAGAGGCTCGGCTGGGCGACA 10673

Qy   1488 CCATGGAGACTGATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGC 1547
          |||||||| | |||||||||||||||||||||||||| | ||||||||||||||||||||
Db  10672 CCATGGAGGCCGATGACCATATGGGTGGCATCCCTGCTCAGAATAGTAAAGGGGAAAGGC 10613

Qy   1548 TTCTGCTTTATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGG 1607
          |||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||
Db  10612 TTCTGCTTTATATTGGCATCATTGACATTCTACAGTCTTACACGTTTCTTAAGAAGTTGG 10553

Qy   1608 AGCACTCTTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCT 1667
          ||||||||||||||||| |||||||||| || ||| ||||||||||||||||||||||||
Db  10552 AGCACTCTTGGAAAGCCGTGGTACATGATGGGGACGCTGTCTCAGTGCATCGCCCAGGCT 10493

Qy   1668 TCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGA 1727
          ||||||||||||||||||||| ||||||||||||| |||||||||||||||| |||||||
Db  10492 TCTACGCTGAACGGTTCCAGCACTTCATGTGCAACGCAGTATTTAAGAAGATCCCCTTGA 10433

Qy   1728 AGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCA 1787
          ||||||||||||||||||||||||||||||||| ||||||||||| ||   | |||||||
Db  10432 AGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTTATCTTTCTCTCTGCATACGGGCTCCA 10373

Qy   1788 GTGGCAACTCCTGCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGA 1847
          |||||||||||||||||||||||||||||| |||||||| |||||||||| ||||||||
Db  10372 GTGGCAACTCCTGCATTACTTACCAGCCATTGGTCTCTGAGGAACACAAGTCACAAGTG- 10314

Qy   1848 CAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGA 1907
            | |||||   ||||||||||||| ||||||||||||||| ||||||||||||||||||
Db  10313 --ATAAAGGTGCAAGTGGAGCCAGGTGTTCACCTTGGTCGTTCTGATGTTTTACCTCAGA 10256

Qy   1908 C-------TCCACCTTTGGAGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTC 1960
          |       ||||||||||||||||||||||||||||||  ||||| |||||| |||||||
Db  10255 CCTCAGAATCCACCTTTGGAGGAAATCAGTGAGGGCTC-ACTATTACTGACCACAGTTTC 10197

Qy   1961 TCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTT 2020
          |||||| |||||||| |||||||||| |||||||||||||||| |||||||||||| |||
Db  10196 TCACCTGTAGTTGGAAAGACTTTGCATATGCTAACTACAAGTATAACCTTGGAAAAACTT 10137

Qy   2021 GAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGA 2080
          |||  | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  10136 GAATGTACAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGA 10077

Qy   2081 TTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTT 2140
          ||||| | |||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  10076 TTCTG-CTTCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAGCAATGTTGAATTTTCTT 10018

Qy   2141 CTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCT 2200
          |||||||||||||||||||||||||||| ||||| |||| |  ||    |||||||||||
Db  10017 CTACTTGGTCATCAAAAAAGGAGTGTAAAAGAAGCGAGGTGCACT----CTCCATCTTCT 9962
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Qy      2201 TCCTGAAGAAGAACCTTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAG 2260
             |||||||||||| ||| || | ||||    ||||||| ||||||| |||||||||  ||
Db      9961 TCCTGAAGAAGAGCCTCCTATTCTTCTCTGTCCTCATAAATGGGCATTAGTGCCTTGGAC 9902

Qy      2261 AGTTGAGGA--------------CCGCAGCATCCCCTCCACTCCAGAGTTGGGTGGTACG 2306
             |||||||||              || |||||||||||||||||||||||||||||| |||
Db      9901 AGTTGAGGACCACTCCATCCTCTCCACAGCATCCCCTCCACTCCAGAGTTGGGTGGCACG 9842

Qy      2307 GATTTTCAACTGGCCAACCCTTTGCCTCCACTATTGAATTTTTTTCAGACCCCCATTCTT 2366
             |||||||||||||| || |||| || ||||| | ||||||||||||||||||||||||||
Db      9841 GATTTTCAACTGGCTAA-CCTTGGCTTCCACAACTGAATTTTTTTCAGACCCCCATTCTT 9783

Qy      2367 CATGCTGGAAATGGGATTGCTGGACTTGGCAGCTTTCTTTCCCCTCGTCTTTGACTAGGA 2426
             ||||||||||||| || | ||||||||||||| ||||||||||||| ||||| || ||||
Db      9782 CATGCTGGAAATGAGACTACTGGACTTGGCAGTTTTCTTTCCCCTCATCTTTCACCAGGA 9723

Qy      2427 ACCGGACTCTTAATTTCCTCAGGACAGACTAGCTGGCACATTATCCCTACCTTAGTTCTT 2486
             || |||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||
Db      9722 ACTGGACTCTTAATTTCCTCAGGACAGACTAGCTGCCACATTATCCCCACCTTAGTTCTT 9663

Qy      2487 TCTCTCTGACTCCTGGAAGAATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATAAGG 2546
             |||||||||  |||||||||| || ||||||||||||||| |||||||||||||||||||
Db      9662 TCTCTCTGATCCCTGGAAGAAAACCCCTGTAATCTCTGTATAGGTTTTTGGGGGATAAGG 9603

Qy      2547 GTGTTTAACCACCTCCCAGCTTTCTTCTTCTTTTTTTTTTCTGAAAAAAGGAAAAAGCAC 2606
             |||||||||||||||||| ||   || || ||||||||| |||||||||||||||||| |
Db      9602 GTGTTTAACCACCTCCCAACT---TTGTTTTTTTTTTTTCCTGAAAAAAGGAAAAAGCGC 9546

Qy      2607 ACAGCACACAATTTCAAGCCATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGATGCCT 2666
             |||||||  |||||||||||| |||||||||| || ||||||||||||||| ||||||||
Db      9545 ACAGCACCAAATTTCAAGCCAGTTTCAGATCAAAAATCCAGAAGTGTTGACGAGATGCCT 9486

Qy      2667 ATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGTTTATGAAGAGAAGAGTAGTGATTGCTC 2726
             || ||||| |||||||||||||||||| ||||||| ||||| ||| ||||||||||||||
Db      9485 ATCCGTAGGGTTCCCTCAGAAGAGCCACGGTGTTTGTGAAGGGAAAAGTAGTGATTGCTC 9426

Qy      2727 TGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTCTCTTGATGAATTTCTTAAGGCTGAAGG 2786
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      9425 TGCCAGAAGCAGCTCCTCTTTAAACTCCTCATCTCTTGATGAATTTCTTAAGGCTGAAGG 9366

Qy      2787 AATGAAGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCAGCCA 2846
             |||| |||||||||||| |||||||||||||| | |||||||||||||| ||||||||||
Db      9365 AATGGAGAGAGTGGGACGTGGGGTAATCTTTACCACTTTTGTTAAAACATGAGGCAGCCA 9306

Qy      2847 TGGGCTGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATAGTAA 2906
             |||| ||||||||||||||||||||| ||||||||||| ||||||||||||||||| | |
Db      9305 TGGGTTGGGAGATCATAGCCCTTCCTGGGCAGAATCCTATTCACTGCCAGGCTATAATGA 9246

Qy      2907 TTATTACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGACTTAC 2966
             |||||||| |||||||||||||||||||||||||||| |||||||||| |||||||||||
Db      9245 TTATTACTGTTTTGCAATTTGAAATATATTCTGGTTGCTTTTCTAAATATGAAGACTTAC 9186

Qy      2967 CAAATGAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTTCCAA 3026
             ||||||||||||||||||||||||| |||||| |||||||||||||| ||||||||||||
Db      9185 CAAATGAATTTTAGATCATTCTCCAAAGGAGA-TTTTTTTGCTCTTCCCATCTTTTCCAA 9127

Qy      3027 CAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAACAGA 3086
             |||||||||||||||||||| |||||||| |||||||||||| ||||||||||||||||
Db      9126 CAGTGTTCTCCTGTTTGTGGTGCTAAGGTGAAGAGGGGACACCTCTGTCTGTTTAACAGG 9067

Qy      3087 CAGTCCATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAGATTC 3146
             |||||| ||||||||||||||||||||||||||||||| ||||||||||||||  |||||
Db      9066 CAGTCCGTATCTGTGAGGCCAGCAAATATTTTCTTAAATTCATGGGGAGACAGTGGATTC 9007

Qy      3147 TTGCCTTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCCCTGTCTTCATGCAGGGAA 3206
             |||||| ||||||||||||||| |||||||||||||||||||  |||||||||||| |||
Db      9006 TTGCCTCGGTGAGGTCATTGCTATGCCATATGTCCTACCCCC--GTCTTCATGCAGAGAA 8949

Qy      3207 GTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCGTCTACAAGAGTTGTGGTTTTCCA 3266
             ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db      8948 GTTGGAAATGGGGGCTACATATGCCCTCTCCTCCCCACCTACAAGAGTTGTGGTTTTCCA 8889

Qy      3267 TCTGATCCTTCCACTCTTGTCAGGGGAAGAAGGGGGCCTGGTATCTCAGGCAGATTGTTG 3326
             ||||||||||||||| |||||||| ||||||||||||||||||||||||||| |||||||
Db      8888 TCTGATCCTTCCACTGTTGTCAGGAGAAGAAGGGGGCCTGGTATCTCAGGCATATTGTTG 8829

Qy      3327 AATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGATAATATGTTAGCCCATACCC 3386
             |||||||||||||||||||||||||||||||||||||||| | || ||||||||||||||
Db      8828 AATTCCTGTTCTATCCCTTCTCTATCCCACCCTGCCTTGACAGTAGGTTAGCCCATACCC 8769

Qy      3387 CAAATAACTGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCA 3446
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8768 CAAATAACTTTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCA 8709

Qy      3447 TG---TTTTTTACAAGAAGGAAAGAATTCTTGCT--ATTTTTTTTTCATAATTTACTATT 3501
             ||   |||||||||||||||||||||    | ||   | |||||||||||||||||||||
Db      8708 TGTTCTTTTTTACAAGAAGGAAAGAAACAATTCTTGCTATTTTTTTCATAATTTACTATT 8649

Qy      3502 TATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATT 3561
             |||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||
Db      8648 TATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTGTAAGGGGTGGAGAGAATATT 8589

Qy      3562 TGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTAC 3621
             ||||||||||||||||||||||||||||||| ||||| ||||||||| || ||||||  |
Db      8588 TGAGGGAGGGCTGGGTCTTAGGGAAAGGAATAGGGAATCAACATTTTAATGAAGTGTCTC 8529

Qy      3622 TATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGG 3681
             ||||||| ||||||||||||  ||| ||| ||||||| ||||||||||||||||||||||
Db      8528 TATTTGCTTCTACTTTGTATCATTCGGAAAAGGCAAATGCAATATAAAAGTGATATATGG 8469

Qy      3682 TTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
             ||||||||||||||||||| || |||||||||
Db      8468 TTTTAATGTAATAAACTTTTATCAGTTATTTA 8437


RESULT 15
PCT-US01-08631-9786
; Sequence 9786, Application PC/TUS0108631
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 21272-049
;  CURRENT APPLICATION NUMBER: PCT/US01/08631
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 9786
;   LENGTH: 2133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIMILAR
;   LOCATION: (422)..(2107)
;   OTHER INFORMATION: 100% homologous to Homo sapiens 68 kDa type I
;   OTHER INFORMATION: phosphatidylinositol-4-phosphate 5-kinase alpha,accession number
;   OTHER INFORMATION: U78576,Smith-Waterman Score=2912.
PCT-US01-08631-9786

  Query Match             54.2%;  Score 2014;  DB 1;  Length 2133;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 2073;  Conservative    0;  Mismatches    0;  Indels   39;  Gaps    2;

Qy         1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        22 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 81

Qy        61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        82 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 141

Qy       121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 201

Qy    181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    202 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 261

Qy    241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    262 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 321

Qy    301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 381

Qy    361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGG 441

Qy    421 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 GCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTC 501

Qy    481 CT---CAGCATCTGGAATCAAGAGACCCATGGCATCTGA--------------------- 516
          ||   ||||||||||||||||||||||||||||||||||
Db    502 CTCAGCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTCTTGGAAGCTAGACAGGA 561

Qy    517 ---------------GGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAG 561
                         |||||||||||||||||||||||||||||||||||||||||||||
Db    562 TTCTTACATCTCATTGGTGCCTTATGCCTCTGGCATGCCCATCAAGAAAATAGGCCATAG 621

Qy    562 AAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGG 621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 AAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGACAACCTCATCAGCCTTGAAAGG 681

Qy    622 TGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGA 681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 TGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCCTGAGTACCAAACCAGAGCGTGA 741

Qy    682 TGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAA 741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 TGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCTTCTTTCCCAGTGAAGGGAGCAA 801

Qy    742 CCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTT 801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    802 CCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTT 861

Qy    802 CCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAG 861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    862 CCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAG 921

Qy    862 TGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAG 921
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    922 TGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAG 981

Qy    922 CGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCT 981
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    982 CGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCT 1041

Qy    982 GCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTA 1041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1042 GCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTA 1101

Qy   1042 TGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCT 1101
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Qy   1102 TTTACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACG 1161
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Qy   1162 GCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTT 1221
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Qy   1222 ACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGAC 1281
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Qy   1702 CACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTTCCAAAAAGTTTCGGTCTGGCTC 1761
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Qy   2002 TACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCT 2061
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Db   2122 CAGAAGACCTGG 2133

Search completed: May 13, 2003, 05:17:29
Job time : 9153 secs
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                         GenCore version 5.1.5
                Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:         May 13, 2003, 02:04:59 ; Search time 494 Seconds
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters:      1567708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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      Pred. No. is the number of results predicted by chance to have a
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      and is derived by analysis of the total score distribution.

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Result            Query
  No.   Score     Match Length DB  ID                        Description
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    2    469.8    12.7     598 10  US-09-864-761-13058         Sequence 13058, A
    3      408    11.0    1899 10  US-09-954-456-827           Sequence 827, App
c   4    356.2     9.6     451  9  US-09-292-758-55           Sequence 55, Appl
    5    312.2     8.4     398  9  US-09-918-995-3253         Sequence 3253, Ap
    6      285     7.7     346 10  US-09-864-761-29620         Sequence 29620, A
    7      152     4.1     350 10  US-09-783-590-9100          Sequence 9100, Ap
    8    102.8     2.8     497  9  US-09-918-995-5650         Sequence 5650, Ap
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   10     73.8     2.0    1266  9  US-10-012-055-3            Sequence 3, Appli
   11     73.8     2.0    3224  9  US-10-012-055-1            Sequence 1, Appli
   12     54.2     1.5     422 10  US-09-878-574-3267          Sequence 3267, Ap
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   14     45.6     1.2    1837 10  US-09-833-381-1934          Sequence 1934, Ap
   15     44.8     1.2     671  9  US-10-184-644-346          Sequence 346, App
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   17       44     1.2    5979  9  US-10-239-676-18           Sequence 18, Appl
   18     43.6     1.2   11812  9  US-10-239-676-210          Sequence 210, App
   19     42.4     1.1     345 10  US-09-783-590-2746          Sequence 2746, Ap
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   21     41.4     1.1   14649  9  US-10-239-676-121          Sequence 121, App
   22     41.2     1.1   41104 10  US-09-816-685-3             Sequence 3, Appli
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c  24     40.8     1.1     457  9  US-09-918-995-15437        Sequence 15437, A
   25     40.4     1.1     468  9  US-09-918-995-3720         Sequence 3720, Ap
   26       40     1.1     594  9  US-10-123-155-10           Sequence 10, Appl
   27     39.8     1.1   15732  9  US-10-239-676-95           Sequence 95, Appl
c  28     39.4     1.1     351 10  US-09-770-791-692           Sequence 692, App
c  29     39.4     1.1     351 10  US-09-924-035A-497          Sequence 497, App
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   33     38.8     1.0    6478  9  US-10-239-676-124          Sequence 124, App
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c  36     38.4     1.0     281  9  US-09-933-797-512          Sequence 512, App
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   42     38.2     1.0  139257  9  US-09-920-671-11           Sequence 11, Appl
c  43     38.2     1.0  640681 10  US-09-790-988-1             Sequence 1, Appli
   44       38     1.0    5127  9  US-10-239-676-131          Sequence 131, App
   45     37.8     1.0    4500 10  US-09-771-003-1             Sequence 1, Appli


                                   ALIGNMENTS


RESULT 1
US-09-998-598-1241/c
; Sequence 1241, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
;  APPLICANT: Stolk, John A.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Chenault, Ruth A.
;  APPLICANT:  Meagher, Madelein Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.561
;  CURRENT APPLICATION NUMBER: US/09/998,598
;  CURRENT FILING DATE:  2001-11-16
;  NUMBER OF SEQ ID NOS: 2606
;  SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1241
;   LENGTH: 553
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-998-598-1241

  Query Match             14.9%;  Score 551.4;  DB 10;  Length 553;
  Best Local Similarity   99.8%;  Pred. No. 6.7e-154;
  Matches  552;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        553 TCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCTGCATTACTTACCAGCCATCGGTCTCTG 494

Qy       1827 GGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTGGTC 1886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 GGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAGCCAGGCGTTCACCTTGGTC 434

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1947 CTGACCCCAGTTTCTCACCTCTAGTTGGAGAGACTTTGCAAATGCTAACTACAAGTACAA 2006
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Qy   2007 CCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGTTCACCCATTAAGCGCAAAGCCTCAGAA 2066
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Qy   2067 GACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCAGCCCTTGCCCCAGCAA 2126
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    253 GACCTGGAACAAGATTCTGCCATCTCTGTGATCCCAAGATGTCGGCCCTTGCCCCAGCAA 194

Qy   2127 TGCTGAATTTTCTTCTACTTGGTCATCAAAAAAGGAGTGTAATAGAAGTGAGGGGAGCTG 2186
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Qy   2307 GATTTTCAACTGG 2319
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RESULT 2
US-09-864-761-13058
; Sequence 13058, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT: Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: PCT/US01/00668
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;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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;   LENGTH: 598
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   OTHER INFORMATION: MAP TO AL096800.20
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
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;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.53
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
US-09-864-761-13058

  Query Match             12.7%;  Score 469.8;  DB 10;  Length 598;
  Best Local Similarity   90.1%;  Pred. No. 1.8e-129;
  Matches  527;  Conservative    0;  Mismatches   52;  Indels    6;  Gaps    2;

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Qy   1391 AC---ACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACA 1447
          ||    ||    ||| | || |||| ||||| ||| ||||||||||||||||||||||||
Db     62 ACTCTTCAAGTGTCAATCGACACTCAAAGACTGGCTCCCCAAAAGGCTCTGTATTCCACA 121

Qy   1448 GCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCAT 1507
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Db    122 GCCATGGAATTCATCCAGGGAGAGGCTCGGCTGGGCGACACCATGGAGGCCGATGACCAT 181

Qy   1508 ATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATC 1567
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Db    182 ATGGGTGGCATCCCTGCTCAGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATC 241

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Qy   1808 TACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAGAAGTGGAG 1867
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RESULT 3
US-09-954-456-827
; Sequence 827, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
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;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 827
;   LENGTH: 1899
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-827

  Query Match             11.0%;  Score 408;  DB 10;  Length 1899;
  Best Local Similarity   67.7%;  Pred. No. 1.2e-110;
  Matches  605;  Conservative    0;  Mismatches  280;  Indels    9;  Gaps    2;

Qy    862 TGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAG 921
          ||| || || || ||||| | || | |||||||| ||||| ||| | || | |||| ||||
Db      1 TGAACCTCTAATAGAACTGTCTAACCCTGGAGCCAGTGGATCCTTGTTTTTTGTGACCAG 60

Qy    922 CGACGATGAGTTCATTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCT 981
           || ||||| || || || || ||||| || || ||||| || || ||||| ||||||||
Db     61 TGATGATGAATTTATCATCAAAACAGTTCAGCACAAAGAAGCTGAGTTTCTTCAGAAGCT 120

Qy    982 GCTTCCAGGATACTACATGAACCTCAACCAGAACCCTCGGACTTTGCTGCCTAAATTCTA 1041
           || ||||| || ||||||||  | |||||||| ||  ||||| |  |||| ||||| ||
Db    121 ACTGCCAGGCTATTACATGAATTTAAACCAGAATCCAAGGACTCTTTTGCCAAAATTTTA 180

Qy   1042 TGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCT 1101
           |||||||| ||| ||||  |||| ||||  || ||  |||||||||||||||||||  |
Db    181 CGGACTGTATTGTATGCAATCAGGAGGCATTAATATCAGGATTGTGGTGATGAACAACGT 240

Qy   1102 TTTACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACG 1161
          ||| ||| | ||  | | ||||||  | | ||||||| | ||||||||||| || || ||
Db    241 TTTGCCACGCTCCATGAGAATGCACTTTACATATGACTTGAAAGGCTCAACGTATAAGCG 300

Qy   1162 GCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTT 1221
            | || ||||  |||||| |||||||  |    |||||||||||| ||| |||| ||| |
Db    301 AAGAGCATCCCGTAAAGAGAGAGAGAAATCCAACCCCACATTTAAGGACTTAGATTTCCT 360

Qy   1222 ACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGAC 1281
           |||||||| |  || ||  | | ||| ||| | || |  |||||||| ||    || ||
Db    361 GCAAGACATGCACGAAGGGTTGTATTTTGATACGGAAACATACAACGCGCTTATGAAAAC 420

Qy   1282 CCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGAT 1341
           || ||| | |||||   ||||||  | ||||||||||| |||||||| |||||  || |
Db    421 ACTTCAGAGAGACTGCCGGGTGCTAGAAAGCTTCAAGATCATGGATTATAGCCTTCTGTT 480

Qy   1342 GTCAATCCATAATATAGATCATGCACAACGAGAGCCCTTAAGCAGTGAAACACAGTACTC 1401
          |  ||| |||    | || ||| | |    ||||                ||||  |
Db    481 GGGAATTCATTTCCTGGACCATTCCCTCAAAGAGAAAGAGGAGGAGACCCCACAAAATGT 540

Qy   1402 AGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCCAT 1461
             |||| ||    |  | |     || |||| ||| || || |||||||||||||| ||
Db    541 GCCTGATGCTAAGCGGACTGGGATGCAGAAGGTTCTCTACTCAACAGCCATGGAATCTAT 600

Qy   1462 CCAG------GGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGG 1515
          ||||      ||  |  || ||   ||    | ||  ||||     |||   ||||| ||
Db    601 CCAGGGTCCAGGGAAATCTGGAGATGGGATAATCACAGAGAACCCAGACACAATGGGAGG 660

Qy   1516 CATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACAT 1575
          ||| || ||    |    ||  || ||||  || ||  | | ||| ||||| ||||||||
Db    661 CATTCCAGCTAAAAGCCATAGGGGAGAAAAACTACTTTTATTTATGGGCATTATTGACAT 720

Qy   1576 TCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGA 1635
          ||| || || || |||||  | |||||||| || || || |||||||| || ||  ||||
Db    721 TCTGCAATCATATAGGTTAATGAAGAAGTTAGAACATTCCTGGAAAGCTCTTGTTTATGA 780

Qy   1636 CGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCAT 1695
           || |||||||| || || ||| | ||| |||| || || ||  | || |     |||||
Db    781 TGGGGACACTGTTTCTGTTCATAGACCAAGCTTTTATGCAGACAGATTTCTTAAGTTCAT 840

Qy   1696 GTGCAACACAGTATTTAAGAAGATTC---CCTTGAAGCCTTCTCCTTCCAAAAA 1746
          |     || ||| || ||||| ||||   | |||||| |||| || || || ||
Db    841 GAATTCCAGAGTTTTCAAGAAAATTCAAGCTTTGAAGGCTTCACCGTCTAAGAA 894

RESULT 4
US-09-292-758-55/c
; Sequence 55, Application US/09292758
; Publication No. US20020197602A1
; GENERAL INFORMATION:
;  APPLICANT: Burmer, Glenna C.
;  APPLICANT: Brown, Joseph P.
;  APPLICANT: LifeSpan BioSciences, Inc.
;  TITLE OF INVENTION: Nucleic Acid Sequences and Proteins
;  TITLE OF INVENTION: Associated With Aging
;  FILE REFERENCE: 017473-001110US
;  CURRENT APPLICATION NUMBER: US/09/292,758
;  CURRENT FILING DATE: 1999-04-14
;  EARLIER APPLICATION NUMBER: US 60/081,887
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
;   LENGTH: 451
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(451)
;   OTHER INFORMATION: n = a,t,c or g
US-09-292-758-55

  Query Match             9.6%;  Score 356.2;  DB 9;  Length 451;
  Best Local Similarity   96.8%;  Pred. No. 1.3e-95;
  Matches  417;  Conservative    0;  Mismatches    8;  Indels    6;  Gaps    5;

Qy   3289 GGGGAAGAAGGGGGCCTGGTATC--TCAGGCAGATTGTTGAATT-CCTGTTCTAT-CCCT 3344
          ||| |  | |||||||||||||||     | |||||||||||||| ||||||||||| ||||
Db    432 GGGAAGAAGGGGGGCCTGGTATCCTCAGGCCAGATTGTTGAATTCCCTGTTCTATCCCCT 373

Qy   3345 TCTCTATCCCA-CCCTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATAT 3403
          ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 TCTCTATCCCACCCCTGCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATAT 313

Qy   3404 TAGACACCC-CCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAG 3462
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 TAGACACCCNCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAG 253

Qy   3463 GAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTT 3522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 GAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTT 193

Qy   3523 ATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAG 3582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 ATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAG 133

Qy   3583 GGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATT 3642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 GGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATT 73
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Qy   3643 GTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAA 3702
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 GTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAA 13

Qy   3703 TGAGTTATTTA 3713
          |||||||||||
Db     12 TGAGTTATTTA 2


RESULT 5
US-09-918-995-3253
; Sequence 3253, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3253
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-918-995-3253

  Query Match             8.4%;  Score 312.2;  DB 9;  Length 398;
  Best Local Similarity   86.6%;  Pred. No. 1.6e-82;
  Matches  344;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy   2792 AGAGAGTGGGACATGGGGTAATCTTTATCCCTTTTGTTAAAACAGGAGGCAGCCATGGGC 2851
          |||||| | ||||||| | | ||||||| |||||||||||| || || ||  || |||||
Db      2 AGAGAGAGAGACATGGCGGACTCTTTATACCTTTTGTTAAAGCACGAAGCCTCCCTGGGC 61

Qy   2852 TGGGAGATCATAGCCCTTCCTAGGCAGAATCCTGTTCACTGCCAGGCTATAGTAATTATT 2911
           | |||| |||| ||||| ||| ||| ||| |||| |||||||||||||||| || ||||
Db     62 CGTGAGACCATATCCCTTTCTACGCATAATGCTGTGCACTGCCAGGCTATAGGAAATATT 121

Qy   2912 ACTATTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGACTTACCAAAT 2971
          ||||||  ||  ||  ||||||||||||| || |||||| || ||||   ||||||||||
Db    122 ACTATTGGGCCCTTACAAATATATTCTGGCTGATTTTCTCAAAGTGACTACTTACCAAAT 181

Qy   2972 GAATTTTAGATCATTCTCCAGAGGAGATTTTTTTTGCTCTTCTCATCTTTTCCAACAGTG 3031
          ||  | |||| ||||||||| |||||||  | |||||| | ||||||| | ||||||| |
Db    182 GAGCTCTAGAGCATTCTCCAAAGGAGATAGTGTTTGCTGTGCTCATCTATCCCAACAGGG 241

Qy   3032 TTCTCCTGTTTGTGGAGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAACAGACAGTC 3091
          || | |||| || || ||||||||||||||||||||||||||||||||||||||||||||
Db    242 TTGTTCTGTGTGAGGGGCTAAGGTAAAGAGGGGACACTTCTGTCTGTTTAACAGACAGTC 301

Qy   3092 CATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAGATTCTTGCC 3151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 CATATCTGTGAGGCCAGCAAATATTTTCTTAAACTCATGGGGAGACAGCAGATTCTTGCC 361

Qy   3152 TTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCC 3188
          |||||||||||||||||||||||||||||||||||||
Db    362 TTGGTGAGGTCATTGCTGTGCCATATGTCCTACCCCC 398


RESULT 6
US-09-864-761-29620
; Sequence 29620, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29620
;   LENGTH: 346
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL096800.20
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.53
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.53
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
;   OTHER INFORMATION: SWISSPROT HIT: P38994, EVALUE 4.00e-07
;   OTHER INFORMATION: NT HIT: gi4505814, EVALUE 1.00e-125
;   OTHER INFORMATION: EST_HUMAN HIT: BE794576.1, EVALUE 1.00e-125
US-09-864-761-29620

  Query Match             7.7%;  Score 285;  DB 10;  Length 346;
  Best Local Similarity   92.3%;  Pred. No. 2e-74;
  Matches  300;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy   1400 TCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATCC 1459
          ||| | || |||| ||||| ||| |||||||||||||||||||||||||||||||||| |
Db     22 TCAATCGACACTCAAAGACTGGCTCCCCAAAAGGCTCTGTATTCCACAGCCATGGAATTC 81

Qy   1460 ATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATC 1519
          ||||||||||||||||| | ||| |  ||||||||| | |||||||||||||||||||||
Db     82 ATCCAGGGAGAGGCTCGGCTGGGCGACACCATGGAGGCCGATGACCATATGGGTGGCATC 141

Qy   1520 CCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTA 1579
          ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 CCTGCTCAGAATAGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTA 201
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Qy   1580 CAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGA 1639
          |||||||||| |||| ||||||||||||||||||||||||||||| |||||||||| ||
Db    202 CAGTCTTACACGTTTCTTAAGAAGTTGGAGCACTCTTGGAAAGCCGTGGTACATGATGGG 261

Qy   1640 GACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGC 1699
          ||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    262 GACGCTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCACTTCATGTGC 321

Qy   1700 AACACAGTATTTAAGAAGATTCCCT 1724
          ||| |||||||||||||||| ||||
Db    322 AACGCAGTATTTAAGAAGATCCCCT 346


RESULT 7
US-09-783-590-9100
; Sequence 9100, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Patrick J.
;  APPLICANT:  Haseltine, William A.
;  APPLICANT:  Li, Haodong
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
;  FILE REFERENCE: PO-16.2C1
;  CURRENT APPLICATION NUMBER: US/09/783,590
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 08/420,856
;  PRIOR FILING DATE: 1995-04-12
;  PRIOR APPLICATION NUMBER: 08/346,731
;  PRIOR FILING DATE: 1994-11-21
;  NUMBER OF SEQ ID NOS: 12485
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9100
;   LENGTH: 350
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (24)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (40)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (44)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (134)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (172)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (173)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (184)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (189)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (193)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (203)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (209)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (217)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (245)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (250)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (256)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (282)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (298)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (317)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (321)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (323)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (350)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-9100

  Query Match              4.1%;  Score 152;  DB 10;  Length 350;
  Best Local Similarity   69.9%;  Pred. No. 1.1e-34;
  Matches  232;  Conservative    0;  Mismatches   95;  Indels    5;  Gaps    3;

Qy   2448 GGACAGACTAGCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACT-CCTGGAAGA 2506
          | ||||||||||||  |||||||||| |||| ||| |||||||||||| | |||||||||
Db      9 GAACAGACTAGCTGCNACATTATCCCCACCTNAGTNCTTTCTCTCTGAATCCCTGGAAGA 68

Qy   2507 ATACTCCTGTAATCTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGC 2566
          | || ||||||||||||||| ||||||||||||||||||||||||||||||||| ||
Db     69 AAACCCCTGTAATCTCTGTACAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTGCCCAA 128

Qy   2567 TTTCTTCTTCTTTTTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCC 2626
           || |  || ||||||||  | |||||| ||||||||  |||||  |  | ||| | |||
Db    129 CTT-TGNTTTTTTTTTTTCCCCGAAAAAGGGAAAAAGGGCACAGNNCCAATTTTAANGCC 187

Qy   2627 ATTTTCAGATCAGAACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGA 2686
          | ||| || ||| || |||||  || |||    | ||||| | ||| |  |||||
Db    188 ANTTTNAGTTCAAAANTCCAGNGGTTTTGNGGGGTTGCCTTTCCGTGGGATTCCCCTNAG 247

Qy   2687 AGAG---CCATGGTGTTTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCT 2743
          |  |   |   | | |||   | | |||  || | | |||  |||||| | |    | |
Db    248 AANGGGCCNGGGTTTTTTTAAAGGGGAAAGGTGGNGTTTGTCCTGCCAAANGGGATTTCC 307

Qy   2744 CTTTAAACTCCTCCTCTCTTGATGAATTTCTT 2775
           ||| || | | |   | |||  | | || ||
Db    308 TTTTTAAATNCCCNANTTTTGGGGGAATTTTT 339


RESULT 8
US-09-918-995-5650
; Sequence 5650, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
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;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5650
;   LENGTH: 497
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(497)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5650

  Query Match             2.8%;  Score 102.8;  DB 9;  Length 497;
  Best Local Similarity   65.5%;  Pred. No. 7.5e-20;
  Matches  182;  Conservative    0;  Mismatches   92;  Indels    4;  Gaps    2;

Qy     1473 CTCGACGGGGTGGTACCATGGAGACTGATGACCATATGGGTGGCATCCCTGCCCGGA-AT 1531
            || ||   ||    ||||  ||||      ||   ||||| ||||| ||  ||   |
Db       76 CTGGAGATGGGATAATCACAGAGAACTTATACACAATGGAGGCATTCCAGCTAAAAGCG 135

Qy     1532 AGTAAAGGGGAAAGGCTTCTGCTTTATATTGGCATCATTGACATTCTACAGTCTTACAGG 1591
             |||  || ||||  || ||  | | ||| ||||| ||||||||||| || || || |||
Db      136 CGTAGGGGAGAAAAACTACTTTTATTTATGGGCATTATTGACATTCTGCAATCATATAGG 195

Qy     1592 TTTGTTAAGAAGTTGGAGCACTCTTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCA 1651
            ||  | |||||||| || || || |||||||| || ||  |||| || |||||||| ||
Db      196 TTAATGAAGAAGTTAGAACATTCCTGGAAAGCTCTTGTTTATGATGGGGACACTGTTTCT 255

Qy     1652 GTGCATCGCCCAGGCTTCTACGCTGAACGGTTCCAGCGCTTCATGTGCAACACAGTATTT 1711
            || ||| | ||| |||| || || ||   | || |     ||||||     || ||| ||
Db      256 GTTCATAGACCAAGCTTTTATGCAGACAGATTTCTTAAGTTCATGAATTCCAGAGTTTTC 315

Qy     1712 AAGAAGATTC---CCTTGAAGCCTTCTCCTTCCAAAAA 1746
            ||||| ||||   | |||||| |||| || || || ||
Db      316 AAGAAAATTCAAGCTTTGAAGGCTTCACCGTCTAAGAA 353

RESULT 9
US-09-938-842A-2662
; Sequence 2662, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2662
;   LENGTH: 2580
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-2662

  Query Match             2.0%;  Score 75;  DB 9;  Length 2580;
  Best Local Similarity   49.2%;  Pred. No. 5.3e-11;
  Matches  325;  Conservative    0;  Mismatches  315;  Indels   21;  Gaps    4;

Qy      716 ATCTTCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGT 775
            || ||||| || || || ||   |||  | |||||| | ||  | |     |||||
Db     1426 ATGTTCTTCCCTAGAGACGGCTCCAATTTACCCCTCCACACAAATCTGTCGACTTCTCC 1485

Qy      776 TTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCC 835
            |  ||   ||||   ||  | |  ||| |  | ||  || || | ||     |     |
Db     1486 TGGAAAGACTATTGTCCCATGGTTTTCAGGAATTTAAGGCAGATGTTCAAGTTAGATGCT 1545

Qy      836 GATGATTACTTGTATTCCCTCTGCAGTGAGCCG---CTGATTGAACTCTGTAGCTCTGGA 892
            |  || ||| ||   ||  | ||  ||||       ||||  ||| | | |  | | ||
Db     1546 GCAGAGTACATGATGTCTATTTGTGGTGATGATGGCCTGACAGAAATTTCTTCCCCCGGG 1605

Qy      893 GCTAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAA 952
               |||||     | |||||  | ||    |||||    ||  | || |||||  |  ||
Db     1606 AAAAGTGGCAGTATCTTCTACCTTTCTCATGACGACAGATTTGTGATCAAGACTTTAAAA 1665

Qy      953 CATAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAG 1012
             |    |||  | |  |||| |  |   || | ||    |||||     |  |   | |
Db     1666 AAGTCTGAGTTGCAGGTTCTACTCAGAATGTTGCCTAAGTACTATGAACATGTAGGCGAC 1725

Qy     1013 AACCCTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGT---GCAGGCAGGTGGC 1069
             |       ||  |  |  | ||||| | |||| |  || |  |    |      | ||
Db     1726 CATGAAAACACACTTATAACCAAATTTTTGGAGTTCACAGAATAACCCTCAAGTGGGGT 1785

Qy     1070 AAGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATC 1129
            || ||  | ||  |||| || |||   ||| | ||    | |    | || || |||
Db     1786 AAAAAGGTACGCTTTGTAGTCATGGGGAATATGTTTTGCACAGAATTGAAGATTCATCGT 1845

Qy     1130 AAATATGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAG 1189
               ||||| || || || |||||     || || |   | |  | ||      |    |
Db     1846 CGTTATGATCTAAAGGGTTCAAC---TCAAGGGAGATTTACTGAAAAGATCAAAATCCAA 1902

Qy     1190 CCTCTTCCCACATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTG 1249
                   ||||||| ||||| ||             ||  |  || |||   ||  | ||
Db     1903 GAGAAGACCACATTGAAAGATCT------------TGATCTAGCTTATGAATTTCATATG 1950

Qy     1250 GATGCTGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAG 1309
            ||        |     | || || |  |||    |  |    ||||| | | |  || |
Db     1951 GACAAGCTGTTACGGGAAGCCCTTTTCAAGCAAATTTACTTAGACTGCTCGTTTTTGGAA 2010

Qy     1310 AGCTTCAAGATAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAA 1369
                | || || || || ||||| || ||  ||  | | |||  || || || ||  |||
Db     2011 TCGCTGAACATCATTGACTACAGTCTTTTACTGGGATTACATTTAGAGCTCCTGGCCAA 2070

Qy     1370 C 1370
            |
Db     2071 C 2071

RESULT 10
US-10-012-055-3
; Sequence 3, Application US/10012055
; Patent No. US20020164750A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel A.
;  APPLICANT:  Rudolph-Owen, Laura A.
;  TITLE OF INVENTION: 56634, A NOVEL HUMAN PHOSPHATIDYLINOSITOL 4-PHOSPHATE 5-KINASE
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREOF
;  FILE REFERENCE: 10448-114001
;  CURRENT APPLICATION NUMBER: US/10/012,055
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: 60/248,325
;  PRIOR FILING DATE: 2000-11-14
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1266
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-055-3

  Query Match             2.0%;  Score 73.8;  DB 9;  Length 1266;
  Best Local Similarity   48.8%;  Pred. No. 7e-11;
  Matches  297;  Conservative    0;  Mismatches  297;  Indels   15;  Gaps    3;

Qy      756 ATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGG 815
            |||    || | | ||    ||||||   |||   ||    | |||| |  || |||| |
Db      278 ATCTGCCCAGTCATTTCAAGTTCAAGGAGTATTGTCCCCAGGTCTTCAGGAACCTCCGTG 337
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Qy     816 AGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTG 875
           | | |||||| ||      | | |||||||||   |||||   | |  | || |  |  |
Db     338 ATCGATTTGGCATTGATGACCAAGATTACTTGGTGTCCCTTACCCGAAACCCCCCCAGCG 397

Qy     876 AACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCA 935
           ||           || ||  |||| |   |  |||  | | |||  |||        |
Db     398 AAAG---------TGAAGGCAGTGATGGTCGCTTCCTTATCTCCTACGATCGGACTCTGG 448

Qy     936 TTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACT 995
           | || ||   |||      | | ||    |      |||| |     ||  |    ||
Db     449 TCATCAAAGAAGTATCCAGTGAGGACATTGCTGACATGCATAGCAACCTCTCCAACTATC 508

Qy     996 ACATGAACCTCAACCAGAACCCTCG---GACTTTGCTGCCTAAATTCTATGGACTGTACT 1052
           ||  | || |     ||  || | |    ||  | |||||  | |||   ||  |||||
Db     509 ACCAGTACATTGTGAAGTGCCATGGCAACACGCTTCTGCCCCAGTTCCTGGGGATGTACC 568

Qy    1053 GTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGAT 1112
           | ||    |  |    | |  |||     ||  | ||||||  |||| | ||
Db     569 GAGTCAGTGTGGACAACGAAGACAGCTACATGCTTGTGATGCGCAATATGTTTAGCCACC 628

Qy    1113 CGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCC 1172
              |     |||| |  || ||||||||||| || ||          |||   ||   |
Db     629 GTCTTCCTGTGCACAGGAAGTATGACCTCAAGGGTTCCCTAGTGTCCCGGGAAGCCAGCG 688

Qy    1173 AGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTACAAGACATCC 1232
           | || ||    |  ||     | |||||  |||| ||  | |||||  |  |  | | ||
Db     689 ATAAGGAAAAGGTTAAAGAATTGCCCACCCTTAAGGATATGGACTTTCTCAACAAGAACC 748

Qy    1233 CTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTG 1292
              | |    | ||   || |  || | | | |    |||     |||  ||| || | |
Db     749 AGAAAGTATATATTGGTGAAGAGGAGAAGAAAATATTTCTGG---AGAAGCTGAAGAGAG 805

Qy    1293 ACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGTCAATCCATA 1352
           |      | | ||   |    | ||||| ||||| ||||||||  || |    |||||
Db     806 ATGTGGAGTTTCTAGTGCAGCTGAAGATCATGGACTACAGCCTTCTGCTAGGCATCCACG 865

Qy    1353 ATATAGATC 1361
           | ||   ||
Db     866 ACATCATTC 874

RESULT 11
US-10-012-055-1
; Sequence 1, Application US/10012055
; Patent No. US20020164750A1
; GENERAL INFORMATION:
;  APPLICANT: Meyers, Rachel A.
;  APPLICANT: Rudolph-Owen, Laura A.
;  TITLE OF INVENTION: 56634, A NOVEL HUMAN PHOSPHATIDYLINOSITOL 4-PHOSPHATE 5-KINASE
;  TITLE OF INVENTION:  FAMILY MEMBER AND USES THEREOF
;  FILE REFERENCE: 10448-114001
;  CURRENT APPLICATION NUMBER: US/10/012,055
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: 60/248,325
;  PRIOR FILING DATE: 2000-11-14
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 3224
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (73)...(1335)
US-10-012-055-1

  Query Match             2.0%;  Score 73.8;  DB 9;  Length 3224;
  Best Local Similarity   48.8%;  Pred. No. 1.4e-10;
  Matches  297;  Conservative    0;  Mismatches  297;  Indels   15;  Gaps    3;

Qy     756 ATCACTACAATGACTTTCGTTTCAAGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGG 815
           |||    || | | ||    ||||||   |||   ||    | |||| |  || |||| |
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Db     350 ATCTGCCCAGTCATTTCAAGTTCAAGGAGTATTGTCCCCAGGTCTTCAGGAACCTCCGTG 409

Qy     816 AGCTATTTGGTATCCGGCCCGATGATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTG 875
           | | |||||| ||      | | |||||||||   |||||   | |  | || |  |  |
Db     410 ATCGATTTGGCATTGATGACCAAGATTACTTGGTGTCCCTTACCCGAAACCCCCCCAGCG 469

Qy     876 AACTCTGTAGCTCTGGAGCTAGTGGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCA 935
           ||           || ||  |||| |   |  |||  | | |||  |||        |
Db     470 AAAG---------TGAAGGCAGTGATGGTCGCTTCCTTATCTCCTACGATCGGACTCTGG 520

Qy     936 TTATTAAGACAGTCCAACATAAAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACT 995
           | || ||   |||      | | ||    |      |||| |     ||  |    ||
Db     521 TCATCAAAGAAGTATCCAGTGAGGACATTGCTGACATGCATAGCAACCTCTCCAACTATC 580

Qy     996 ACATGAACCTCAACCAGAACCCTCG---GACTTTGCTGCCTAAATTCTATGGACTGTACT 1052
           ||  | || |     ||  || | |    ||  | |||||  | |||   ||  |||||
Db     581 ACCAGTACATTGTGAAGTGCCATGGCAACACGCTTCTGCCCCAGTTCCTGGGGATGTACC 640

Qy    1053 GTGTGCAGGCAGGTGGCAAGAACATTCGGATTGTGGTGATGAACAATCTTTTACCAAGAT 1112
           | ||    |  |    | |  |||     ||  | ||||||  |||| | ||
Db     641 GAGTCAGTGTGGACAACGAAGACAGCTACATGCTTGTGATGCGCAATATGTTTAGCCACC 700

Qy    1113 CGGTAAAAATGCATATCAAATATGACCTCAAAGGCTCAACCTACAAACGGCGGGCTTCCC 1172
              |     |||| |  || ||||||||||| || ||          |||   ||   |
Db     701 GTCTTCCTGTGCACAGGAAGTATGACCTCAAGGGTTCCCTAGTGTCCCGGGAAGCCAGCG 760

Qy    1173 AGAAAGAGCGAGAGAAGCCTCTTCCCACATTTAAAGACCTAGACTTCTTACAAGACATCC 1232
           | || ||    |  ||     | |||||  |||| ||  | |||||  |  |  | | ||
Db     761 ATAAGGAAAAGGTTAAAGAATTGCCCACCCTTAAGGATATGGACTTTCTCAACAAGAACC 820

Qy    1233 CTGATGGTCTTTTTTTGGATGCTGACATGTACAACGCTCTCTGTAAGACCCTGCAGCGTG 1292
              | |    | ||   || |  || | | | |    |||     |||  ||| || | |
Db     821 AGAAAGTATATATTGGTGAAGAGGAGAAGAAAATATTTCTGG---AGAAGCTGAAGAGAG 877

Qy    1293 ACTGTTTGGTGCTGCAGAGCTTCAAGATAATGGATTACAGCCTCTTGATGTCAATCCATA 1352
           |      | | ||   |    | ||||| ||||| ||||||||  || |    |||||
Db     878 ATGTGGAGTTTCTAGTGCAGCTGAAGATCATGGACTACAGCCTTCTGCTAGGCATCCACG 937

Qy    1353 ATATAGATC 1361
           | ||   ||
Db     938 ACATCATTC 946

RESULT 12
US-09-878-574-3267
; Sequence 3267, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT:  La Rosa, Thomas J.
;  APPLICANT:  Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(15401)B
;  CURRENT APPLICATION NUMBER: US/09/878,574
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 09/333,535
;  PRIOR FILING DATE: 1999-06-14
;  NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3267
;   LENGTH: 422
;   TYPE: DNA
;   ORGANISM: Glycine max
;   OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-E8
US-09-878-574-3267

  Query Match             1.5%;  Score 54.2;  DB 10;  Length 422;
  Best Local Similarity   52.4%;  Pred. No. 2.2e-05;
  Matches  144;  Conservative    0;  Mismatches  128;  Indels    3;  Gaps    1;

Qy     722 TTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAG 781
           ||||| |  |||||     |  | || ||| ||||||| |   |||| |||   |  ||
Db      52 TTTCCTAAAGAAGGTTCTCAATTAACACCTACTCATCAGTCAGATGATTTTAAATGGAAA 111
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Qy    782 ACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGAT 841
             |||   ||  | |  ||     | ||  |  | ||  |    ||     | |  |||
Db    112 GATTATTGTCCCATGGTGTTTAAGAATTTGAGAAAACTGGTCAAGATTGATGCTGCCGAT 171

Qy    842 TACTTGTATTCCCTCT---GCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGT 898
          ||| ||   ||| | |   | |  ||  | ||||  ||||| | |    | ||    |||
Db    172 TACATGATGTCCATTTGTGGAAACGATACTCTGAGGGAACTATCTTCTCCGGGGAAAAGT 231

Qy    899 GGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAA 958
          |||    | |||    ||||    || |||   ||||| || |||||| | | |
Db    232 GGTAGTGTCTTCCTCCTGTCTCAAGATGATCGTTTCATGATCAAGACACTGCGAAGATTT 291

Qy    959 GAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATA 993
          || |   || | ||    |   |||||||||  ||
Db    292 GAAGTCAAAGTCCTTTCAAGAATGCTTCCAGACTA 326

RESULT 13
US-09-878-574-3268
; Sequence 3268, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT:  La Rosa, Thomas J.
;  APPLICANT:  Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(15401)B
;  CURRENT APPLICATION NUMBER: US/09/878,574
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 09/333,535
;  PRIOR FILING DATE: 1999-06-14
;  NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3268
;   LENGTH: 337
;   TYPE: DNA
;   ORGANISM: Glycine max
;   OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-E9
US-09-878-574-3268

  Query Match             1.4%;  Score 52.6;  DB 10;  Length 337;
  Best Local Similarity   52.0%;  Pred. No. 5.6e-05;
  Matches  143;  Conservative    0;  Mismatches  129;  Indels    3;  Gaps    1;

Qy    722 TTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCAAG 781
          ||||| |  |||||     |  | || ||| ||||| | |   |||| |||   |  ||
Db     52 TTTCCTAAAGAAGGTTCTCAATTAACACCTACTCATGAGTCAGATGATTTTAAATGGAAA 111

Qy    782 ACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATGAT 841
             |||   |   | |  ||  |  | ||  | ||||| ||    ||     | |  |||
Db    112 GATTATTGTCTCATGGTGTTTAGAAATTTGAGAGAGCTGTTCAAGATTGATGCTGCCGAT 171

Qy    842 TACTTGTATTCCCTCTGCAGT---GAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGT 898
          ||| ||   ||| | ||  |    ||  | ||||  ||||| | |    | ||    |||
Db    172 TACATGATGTCCATTTGTGGAAACGATACTCTGAGGGAACTATCTTCTCCGGGGAAAAGT 231

Qy    899 GGTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAA 958
          |||    | ||||   ||||    || |||   ||||| || || ||| | | |
Db    232 GGTAGTGTCTTCTTCCTGTCTCAGGATGATCGTTTCATGATCAATACATTGCGAAGATCT 291

Qy    959 GAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATA 993
          ||     |  | || |      ||| |||||  ||
Db    292 GAATTCAAGGTCCTTCTATTAATGCGTCCAGACTA 326

RESULT 14
US-09-833-381-1934
; Sequence 1934, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1934
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1837)
;   OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1934

  Query Match             1.2%;  Score 45.6;  DB 10;  Length 1837;
  Best Local Similarity   50.4%;  Pred. No. 0.025;
  Matches  139;  Conservative    0;  Mismatches  134;  Indels    3;  Gaps    1;

Qy   1086 TGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACCTCAAAG 1145
          | ||||||  |||| | ||           |     |||| |  || ||||||||||| |
Db      4 TTGTGATGCGCAATATGTTTAGCCACCGTCTTCCTGTGCACAGGAAGTATGACCTCAAGG 63

Qy   1146 GCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCACATTTA 1205
          | ||          |||   ||   | | || ||    |  ||     | |||||  |||
Db     64 GTTCCCTAGTGTCCCGGGAAGCCAGCGATAAGGAAAAGGTTAAAGAATTGCCCACCCTTA 123

Qy   1206 AAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACATGTACA 1265
          | ||  | |||||  |  |  | | ||   | |    | ||   || |  || |   | |
Db    124 AGGATATGGACTTTCTCAACAAGAACCAGAAAGTATATATTGGTGAAGAGGAGAAAAAAA 183

Qy   1266 ACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGATAATGG 1325
              |||     |||  ||| || | ||      | | ||   |    | ||||| ||||
Db    184 TATTTCTGG---AGAAGCTGAAGAGAGATGTGGAGTTTCTAGTGCAGCTGAAGATCATGG 240

Qy   1326 ATTACAGCCTCTTGATGTCAATCCATAATATAGATC 1361
          | ||||||||  || |    |||||  | ||   ||
Db    241 ACTACAGCCTTCTGCTAGGCATCCACGACATCATTC 276

RESULT 15
US-10-184-644-346
; Sequence 346, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C227
;  CURRENT APPLICATION NUMBER: US/10/184,644
;  CURRENT FILING DATE:  2002-06-28
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 346
;   LENGTH: 671
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-184-644-346

  Query Match             1.2%;  Score 44.8;  DB 9;  Length 671;
  Best Local Similarity   6.2%;  Pred. No. 0.02;
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  Matches   24;  Conservative  150;  Mismatches  215;  Indels    0;  Gaps    0;

Qy    132 CTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAGGGGGTGCGGGA 191
          :: : | :: :    :   : : :  : :    ::  ::|   |  | :::::  : ::
Db    175 SDLDQASVSPSEEENSESSSESEKTSDQDFTPEKKAAVRAPRRGPLGGRKKKKAPSASDS 234

Qy    192 CGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCCAGGAGCCGGCT 251
           :: :::  :   : : ::  ::::   :::::::: :  :| :       : :  :
Db    235 DSKADSDGAKPEPVAMARSASSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRKPKP 294

Qy    252 CGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAACGCGGGTTCTG 311
           :  : : :::::: ::: :  ::::  : :   |:: :      :: :   :  :   :
Db    295 ERPPSSSSSDSDSDEVDRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRR 354

Qy    312 TAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATTGAAAGAGAGCC 371
           :|::  | :  ||:  :    ::  : ::|: |:|:     : :       : |: :
Db    355 ERADRGEAERGSGGSSGDELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAK 414

Qy    372 AGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGGGCCGTCGTCTT 431
             :::   |:: |   ::::      |:  :: :| :::   :   ::   :  :   :
Db    415 KPQSSSTEPARKPGQKEKRVRPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEK 474

Qy    432 CGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGTCCTCAGCATCTG 491
            : ::  :    ::: : ::        ||  :|     :      |  : :::   ::
Db    475 LQKLHSEIKFALKVDSPDVKRCLNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKD 534

Qy    492 GAATCAAGAGACCCATGGCATCTGAGGTG 520
          :: : | :  :  ::  |     : :: :
Db    535 VMEKAAEVYTRLKSRVLGPKIEAVQKVNK 563

Search completed: May 13, 2003, 05:22:52
Job time : 514 secs
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                    GenCore version 5.1.5
          Copyright (c) 1993 - 2003  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:          May 13, 2003, 00:45:33 ; Search time 185 Seconds
                                             (without alignments)
                                             6155.085 Million cell updates/sec

Title:           US-10-003-354-3
Perfect score:   3713
Sequence:        1 attaacaggccgtggttagg..........aaactttaatgagttattta 3713

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued_Patents_NA:*
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                  2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                  3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                   %
Result            Query
  No.    Score   Match Length DB  ID                            Description
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    1     55.4    1.5    7218  1  US-08-232-463-14               Sequence 14, Appl
c   2     51.4    1.4    7218  1  US-08-232-463-14               Sequence 14, Appl
c   3     42.6    1.1     731  1  US-08-451-405A-2               Sequence 2, Appli
    4     38.2    1.0   87350  3  US-08-781-891-79               Sequence 79, Appl
    5     38.2    1.0   87543  4  US-09-791-211-3                Sequence 3, Appli
    6     37.8    1.0    1086  4  US-09-134-001C-1208            Sequence 1208, Ap
c   7     37.6    1.0     624  4  US-09-397-992A-3               Sequence 3, Appli
c   8       36    1.0     624  4  US-09-397-992A-6               Sequence 6, Appli
    9       36    1.0    1983  4  US-09-453-702B-36              Sequence 36, Appl
c  10       36    1.0   53526  3  US-08-658-136-2                Sequence 2, Appli
c  11       36    1.0   53577  3  US-08-658-136-1                Sequence 1, Appli
   12     35.8    1.0     549  4  US-09-118-442-26               Sequence 26, Appl
   13     35.8    1.0     549  4  US-09-677-064-26               Sequence 26, Appl
c  14     35.8    1.0    1164  4  US-09-134-001C-2534            Sequence 2534, Ap
c  15     35.8    1.0    1166  4  US-09-072-596-323              Sequence 323, App
c  16     35.8    1.0    3095  6  5231168-1                     Patent No. 5231168
c  17     35.8    1.0   19124  2  US-08-487-826B-13              Sequence 13, Appl
c  18     35.6    1.0   26385  4  US-08-961-527-3                Sequence 3, Appli
c  19     35.4    1.0    1590  3  US-08-747-221B-23              Sequence 23, Appl
c  20     35.4    1.0    1590  4  US-09-005-051-23               Sequence 23, Appl
c  21     35.4    1.0    1650  3  US-08-747-221B-21              Sequence 21, Appl
   22     35.4    1.0    1650  3  US-08-747-221B-22              Sequence 22, Appl
c  23     35.4    1.0    1650  4  US-09-005-051-21               Sequence 21, Appl
   24     35.4    1.0    1650  4  US-09-005-051-22               Sequence 22, Appl
c  25     35.4    1.0    1792  3  US-08-747-221B-18              Sequence 18, Appl
   26     35.4    1.0    1792  3  US-08-747-221B-20              Sequence 20, Appl
c  27     35.4    1.0    1792  4  US-09-005-051-18               Sequence 18, Appl
   28     35.4    1.0    1792  4  US-09-005-051-20               Sequence 20, Appl
c  29     35.4    1.0    2219  5  PCT-US93-07213-4               Sequence 4, Appli
c  30     35.4    1.0    2870  5  PCT-US93-07213-3               Sequence 3, Appli
c  31     35.4    1.0    3102  5  PCT-US93-07213-1               Sequence 1, Appli
c  32       35    0.9     865  4  US-09-040-984-71               Sequence 71, Appl
c  33       35    0.9     865  4  US-09-123-912-71               Sequence 71, Appl
c  34       35    0.9     865  4  US-09-643-597-71               Sequence 71, Appl
   35       35    0.9    1969  1  US-08-356-340-1                Sequence 1, Appli
   36       35    0.9    1969  2  US-08-786-555-1                Sequence 1, Appli
   37       35    0.9    2566  2  US-08-488-940-19               Sequence 19, Appl
c  38     34.6    0.9   35081  2  US-08-752-760A-1               Sequence 1, Appli
c  39     34.4    0.9    1766  4  US-08-961-527-235              Sequence 235, App
   40     34.2    0.9    2659  3  US-08-749-522-1                Sequence 1, Appli
   41     34.2    0.9    2755  3  US-08-749-522-2                Sequence 2, Appli
   42     34.2    0.9   56516  2  US-08-996-306-1                Sequence 1, Appli
   43     34.2    0.9   56516  4  US-09-338-907-1                Sequence 1, Appli
   44     34.2    0.9   56516  4  US-09-218-207-1                Sequence 1, Appli
   45       34    0.9     421  4  US-08-642-274D-55              Sequence 55, Appl


                                  ALIGNMENTS


RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.5%;  Score 55.4;  DB 1;  Length 7218;
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  Best Local Similarity   1.3%;  Pred. No. 9.5e-06;
  Matches    5;  Conservative  228;  Mismatches  144;  Indels    0;  Gaps    0;

Qy    2216 TTCTCTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAG 2275
           |::::::::::::::::::: :   :   ::::  : ::::      ::     :: :
Db    1066 TYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1125

Qy    2276 CATCCCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCC 2335
           : :::::::: ::::    ::   :  : :   :::::  ::  ::  :::::: :::::
Db    1126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1185

Qy    2336 ACTATTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGG 2395
            :: ::   ::::::::   ::::: :::::: : ::     :    :: ::   :::
Db    1186 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1245

Qy    2396 CAGCTTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGAC 2455
           :  :::::::::::::: :::::  ::     ::   :::::  :::::::    :   :
Db    1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1305

Qy    2456 TAGCTGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTG 2515
           :  ::  : : :: ::::: ::::  ::::::::::::  :::::       : :::::
Db    1306 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1365

Qy    2516 TAATCTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTT 2575
           :  ::::: :     :::::      :     : :::  :: ::::::  ::::::::::
Db    1366 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1425

Qy    2576 CTTTTTTTTTCTGAAA 2592
           :::::::::  |   |||
Db    1426 YYYYYYYYYGTACCAAA 1442


RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.4%;  Score 51.4;  DB 1;  Length 7218;
  Best Local Similarity   5.4%;  Pred. No. 0.00015;
  Matches   16;  Conservative  171;  Mismatches  112;  Indels    0;  Gaps    0;

Qy     136 GAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAGGGGGTGCGGGACGTG 195
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Db    1331 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1272

Qy     196 AGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCCAGGAGCCGGCTCGAC 255
           ::         : :  ::: ::: :: : ::    :::  ::   :::::  ::   ::
Db    1271 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1212

Qy     256 GTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAACGCGGGTTCTGTAAA 315
           : :   ::::::::   :::::::: ::::::: ::   : :::: : :::    : :::
Db    1211 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1152

Qy     316 GAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATTGAAAGAGAGCCAGGC 375
           :::: :  :::::::   ::    ::::::::::::::  :::  :::::::::  :::
Db    1151 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1092

Qy     376 CGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCGGGCCGTCGTCTTCGG 434
            :  :::::::::::::  :  :::|| ||     ||  |  |  || | |    ||||
Db    1091 RRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTCGG 1033


RESULT 3
US-08-451-405A-2/c
; Sequence 2, Application US/08451405A
; Patent No. 5736358
;  GENERAL INFORMATION:
;    APPLICANT:  FASEL, NICOLAS JOSEPH
;    APPLICANT:  REYMOND, CHRISTOPHE DOMINIQUE
;    TITLE OF INVENTION:  DICTYOSTELID EXPRESSION VECTOR AND
;    TITLE OF INVENTION:  METHOD FOR EXPRESSING A DESIRED PROTEIN
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THE WEBB LAW FIRM
;      STREET:  700 KOPPERS BUILDING, 436 SEVENTH AVENUE
;      CITY:  PITTSBURGH
;      STATE:  PENNSYLVANIA
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  15219-1818
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" FLOPPY DISK
;      COMPUTER:  Midwest Micro 486-50
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  WORDPERFECT 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/451,405A
;      FILING DATE:  26-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,273
;      FILING DATE:  15-JAN-1993
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  731
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  UNKNOWN
US-08-451-405A-2

  Query Match             1.1%;  Score 42.6;  DB 1;  Length 731;
  Best Local Similarity  48.5%;  Pred. No. 0.014;
  Matches  117;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;
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Qy    3470 TTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGG 3529
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Db     281 TTTTTTTTTTTTTTTTGGTTGTTGTTTCCAATCCAAAAATTATCTGAATTTTTTTTTTAGA 222

Qy    3530 ACAGAGTTCTGTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGG 3589
           |     || |  ||              |||||   ||    ||  || | |   ||
Db     221 ATTTTCTTATCATATACCGTCACAAATCTATTTTTAGGTTCACTATGTTTAATATAATTT 162

Qy    3590 AATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGA 3649
            |     ||  || |  |   | || |   | |||||   |||| ||| |||| || | |
Db     161 TAAATACAAATAAAAACTCCTTCAAATAGAAATATTTTATTCTAATTTTTATTTTTTAAA 102

Qy    3650 AATGGCAAATACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTA 3709
           ||    |||   || ||||||   |   |        || || ||| |    || | | |
Db     101 AAAATAAAAATAAAAATAAAAAAAAGGAAAAAAAAACATATACTAATCAAATATTATTCA 42

Qy    3710 T 3710
           |
Db      41 T 41

RESULT 4
US-08-781-891-79
; Sequence 79, Application US/08781891
; Patent No. 6090620
;  GENERAL INFORMATION:
;    APPLICANT:  Fu, Ying-Hui
;    APPLICANT:  Yu, Chang-En
;    APPLICANT:  Oshima, Junko
;    APPLICANT:  Mulligan, John T.
;    APPLICANT:  Schellenberg, Gerald D.
;    TITLE OF INVENTION:  GENE AND GENE PRODUCTS RELATED TO
;    TITLE OF INVENTION:  WERNER'S SYNDROME
;    NUMBER OF SEQUENCES:  209
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,891
;      FILING DATE:  27-DEC-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6090620tenburg Ph.D., Carol
;      REGISTRATION NUMBER:  39,317
;      REFERENCE/DOCKET NUMBER:  240052.419
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  79:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-781-891-79

  Query Match              1.0%;  Score 38.2;  DB 3;  Length 87350;
  Best Local Similarity   47.0%;  Pred. No. 7.8;
  Matches  118;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy    3449 TTTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATG 3508
           ||| |   | |||| ||  |||  |   || ||| |||   ||||||   | |    |||
Db   45681 TTTATAGTATGAAGAAATTAATCATACATAGTTTATTTATCTAATTTCTAAATACCCATG 45740
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Qy    3509 TATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGGAGGGAATATTTGAGGGA 3568
            |   || ||  ||     | |   |||| |||      |||    || | |  ||
Db   45741 GAAGAAAATGAATTTAATGGAATGTAGTTGTGTATTACTTGGTTTCGAGTGTGGGAAAAT 45800

Qy    3569 GGGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGC 3628
                 ||||||    |||       |  || |  | |   ||      |   |||
Db   45801 TTATATGGTCTTTCTAAAACAGCACTGTCAGTAGAAATACAATGTGAGCTACATATGCAA 45860

Qy    3629 CTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGTTTTAAT 3688
            | ||  || | | ||    | ||   ||| |  | ||  | |  || |||  |  ||||
Db   45861 TTTTAAATTTTCTAGTAGCCACATTTTAAAAAGTAAATGGATGCAATTTATTTTGATAAT 45920

Qy    3689 GTAATAAACTT 3699
            ||||  | ||
Db   45921 ATAATTTAATT 45931

RESULT 5
US-09-791-211-3
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
;  APPLICANT:  Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION:. ANTISENSE MODULATION OF WRN EXPRESSION
;  FILE REFERENCE:  RTS-0205
;  CURRENT APPLICATION NUMBER: US/09/791,211
;  CURRENT FILING DATE:  2001-02-23
;  NUMBER OF SEQ ID NOS:  90
; SEQ ID NO 3
;   LENGTH: 87543
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 7421
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 7427
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 11609
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 12605
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;   LOCATION: 12742
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;   NAME/KEY: unsure
;   LOCATION: 31205
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;   NAME/KEY: unsure
;   LOCATION: 79134
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 79198
;   OTHER INFORMATION: unknown
;   NAME/KEY: unsure
;   LOCATION: 86336
;   OTHER INFORMATION: unknown
;   OTHER INFORMATION:
US-09-791-211-3

  Query Match             1.0%;  Score 38.2;  DB 4;  Length 87543;
  Best Local Similarity   47.0%;  Pred. No. 7.8;
  Matches  118;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy   3449 TTTTTACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTTCATAATTTACTATTTATGATG 3508
          ||| |   | |||| ||  |||  |   || ||| |||   ||||||   | |    |||
Db  45874 TTTATAGTATGAAGAAATTAATCATACATAGTTTATTTATCTAATTTCTAAATACCCATG 45933

Qy   3509 TATTTAAGTGTTTTATTAAGGACAGAGTTCTGTTAGGGGTGGAGGGAATATTTGAGGGA 3568
           |   || ||  ||     | |   |||| |||      |||    || | |  ||
Db  45934 GAAGAAAATGAATTTAATGGAATGTAGTTGTGTATTACTTGGTTTCGAGTGTGGGAAAAT 45993

Qy   3569 GGCTGGGTCTTAGGGAAAGGAATGGGGAAGCAACATTTTTATTAAGTGTTACTATTTGC 3628
                ||||||    |||       |  || |  | |   ||      |   |||
Db  45994 TTATATGGTCTTTCTAAAACAGCACTGTCAGTAGAAATACAATGTGAGCTACATATGCAA 46053

Qy   3629 CTCTACTTTGTATTGTTCAGAAATGGCAAATACAATATAAAAGTGATATATGGTTTTAAT 3688
           | ||  || | | ||    | ||   ||| |  | ||  | |  || |||  |  ||||
Db  46054 TTTTAAATTTCTAGTAGCCACATTTTAAAAAGTAAATGGATGCAATTTATTTTGATAAT 46113

Qy   3689 GTAATAAACTT 3699
           ||||  | ||
Db  46114 ATAATTTAATT 46124


RESULT 6
US-09-134-001C-1208
; Sequence 1208, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1208
;   LENGTH: 1086
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1208
```

```
  Query Match             1.0%;  Score 37.8;  DB 4;  Length 1086;
  Best Local Similarity   55.8%;  Pred. No. 0.51;
  Matches   72;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy   2916 TTTTGCAATTTGAAATATATTCTGGTTGTTTTTCTAAATGTGAAGACTTACCAAATGAAT 2975
          | || || | | | |  ||| | | |  || |||||  |   |  | |||| |||| |||
Db    385 TATTTCATTATCATAATTATGCAGTTCTTTGTTCTATCTTATATCATTTACAAAATTAAT 444

Qy   2976 TTTAGATCATTCTCCAGAGGAGATTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCT 3035
          |||||||  |||   ||   |  |||  |    |   |    | |  ||||||| | || |
Db    445 TTTAGATTGTTCAATAGTAAAATTTTGCTGCTTTTAGCATTTATAGTCCAACAATCTTAT 504

Qy   3036 CCTGTTTGT 3044
          |    || |
Db    505 CTACATTAT 513


RESULT 7
US-09-397-992A-3/c
; Sequence 3, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46
;  CURRENT APPLICATION NUMBER: US/09/397,992A
;  CURRENT FILING DATE:  1999-09-16
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 624
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: This degenerate sequence encodes the amino acid
;   OTHER INFORMATION: sequence of SEQ ID NO:2.
;   NAME/KEY: variation
;   LOCATION: (1)...(624)
;   OTHER INFORMATION: n is any nucleotide
US-09-397-992A-3

  Query Match             1.0%;  Score 37.6;  DB 4;  Length 624;
  Best Local Similarity   27.2%;  Pred. No. 0.4;
  Matches   72;  Conservative   60;  Mismatches  130;  Indels    3;  Gaps    1;

Qy   3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
          |:||:  |   | :||    :::  :|      :: |  : : :||:| :| :||  :
Db    310 TYTCYTCCCANCCRTCNARNSWDATRTTNGCNCKRAANARNSWRAADATYTGYTGNARCA 251

Qy   3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540
          |:|  |  | :||     :  |:||   : |:|    :| :| :|  ||  :: |:   :
Db    250 TYTCRTGNARDATNGCNARNGTRTGNCCYTTYT---GRTAYTGYTGNGGNSWNARNSWYT 194

Qy   3541 TTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600
          |: | ||  : |:: |:| :||  ::   ||  ::  :|   |:|  :  |  |
Db    193 TYTGNGGNARNARRAARTTYTTNCKRTGNGGNARRCAYTGYTGDATNSWNARNGTYTGNA 134

Qy   3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660
          :    ||  :  :  |    :: | :   |  ||:|    :||:| : |:||:   |::
Db    133 RYTTRTTNARNARYTTNARNSWYTCYTGRTTNACYTGNCKYTGYTGRAADATDATNARYT 74

Qy   3661 CAATATAAAAGTGATATATGGTTTT 3685
            | :|  |:   : |:|| ||  |
Db     73 TNARRTCNARNSWRAADATNGTNGT 49

RESULT 8
US-09-397-992A-6/c
; Sequence 6, Application US/09397992A
; Patent No. 6329175
; GENERAL INFORMATION:
;  APPLICANT: Conklin, Darrell
;  APPLICANT:  Grant, Francis J.
;  APPLICANT:  Rixon, Mark W.
;  APPLICANT:  Kindsvogel, Wayne
;  TITLE OF INVENTION: Interferon-epsilon
;  FILE REFERENCE: 98-46
;  CURRENT APPLICATION NUMBER: US/09/397,992A
;  CURRENT FILING DATE:  1999-09-16
;  PRIOR APPLICATION NUMBER: 60/101,012
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: 60/118,578
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: 60/142,766
;  PRIOR FILING DATE: 1999-07-08
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 624
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: This degenerate sequence encodes the amino acid
;   OTHER INFORMATION: sequence of SEQ ID NO:5.
;   NAME/KEY: variation
;   LOCATION: (1)...(624)
;   OTHER INFORMATION: n is any nucleotide
US-09-397-992A-6

  Query Match             1.0%;  Score 36;  DB 4;  Length 624;
  Best Local Similarity   26.8%;  Pred. No. 1.2;
  Matches   71;  Conservative   60;  Mismatches  131;  Indels    3;  Gaps    1;

Qy   3421 TTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTATT 3480
          |:||:  |   | :||    :::  :|      :: |  : : :||:| :| :||  :
Db    310 TYTCYTCCCANCCRTCNARNSWDATRTTNGCNCKRAANARNSWRAADATYTGYTGNARCA 251

Qy   3481 TTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCTG 3540
          |:|  |  | :||     :   :||   : |:|    :| :| :|  ||  :: |:   :
Db    250 TYTCRTGNARDATNGCNARNGCRTGNCCYTTYT---GRTAYTGYTGNGGNSWNARNSWYT 194

Qy   3541 TTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAGC 3600
          |: | ||  : |:: |:| :||  ::   ||  ::  :|   |:|  :  |  |
Db    193 TYTGNGGNARNARRAARTTYTTNCKRTGNGGNARRCAYTGYTGDATNSWNARNGTYTGNA 134

Qy   3601 AACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAATA 3660
          :    ||  :  :  |    :: | :   |  ||:|    :||:| : |:||:   |::
Db    133 RYTTRTTNARNARYTTNARNSWYTCYTGRTTNACYTGNCKYTGYTGRAADATDATNARYT 74

Qy   3661 CAATATAAAAGTGATATATGGTTTT 3685
            | :|  |:   : |:|| ||  |
Db     73 TNARRTCNARNSWRAADATNGTNGT 49


RESULT 9
US-09-453-702B-36
; Sequence 36, Application US/09453702B
; Patent No. 6365723
;   GENERAL INFORMATION:
;        APPLICANT: Blattner, Frederick R.
;                   Burland,     Valerie
;                   Perna,  Nicole T.
;                   Plunkett, Guy
;                   Welch,  Rod
;        TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
;        NUMBER OF SEQUENCES: 265
```

```
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Quarles & Brady
;              STREET: 1 South Pinckney Street
;              CITY: Madison
;              STATE: WI
;              COUNTRY: US
;              ZIP: 53701-2113
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: Word Perfect 8.0
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/453,702B
;              FILING DATE: 03-Dec-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 60/110,955
;              FILING DATE: 04-DEC-1998
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Seay, Nicholas J.
;              REGISTRATION NUMBER: 27386
;              REFERENCE/DOCKET NUMBER: 960296.95017
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (608) 251-5000
;              TELEFAX: (608) 251-9166
;    INFORMATION FOR SEQ ID NO: 36:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1983
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: DNA  (genomic)
;         SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-453-702B-36

  Query Match             1.0%;  Score 36;  DB 4;  Length 1983;
  Best Local Similarity   52.7%;  Pred. No. 2.7;
  Matches   78;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy   3395 TGTCTATATTAGACACCCCCAGCCAGTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTT 3454
          ||| ||||||  | |    ||      || |  |||| | | |||  ||   |  ||  ||
Db    477 TGTATATATTTAAAAAATTCATTATACTTTTTCCTGCTTATTTTTTCTTGAAGATTCATT 536

Qy   3455 ACAAGAAGGAAAGAATTCTTGCTATTTTTTTTTCATAATTTACTATTTATGATGTATTTA 3514
           |  ||  |||    |||||   ||  |  ||  | ||  ||  |||   ||| | ||
Db    537 GCGCGATTGAATATTTTCTTTAAATGCTGATTGTAGAAAATAAAATTATCGATATCTTGT 596

Qy   3515 AGTGTTTTATTAAGGACAGAGTTCTGTT 3542
            | ||||| |||     || || | ||
Db    597 TTTATTTTAATAACTGTTGATTTTTCTT 624

RESULT 10
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
;  GENERAL INFORMATION:
;    APPLICANT:  KLINGER, KATHERINE W
;    APPLICANT:  LANDES, GREGORY M
;    APPLICANT:  BURN, TIMOTHY C
;    APPLICANT:  CONNORS, TIMOTHY D
;    APPLICANT:  DACKOWSKI, WILLIAM
;    APPLICANT:  GERMINO, GREGORY
;    APPLICANT:  QIAN, FENG
;    TITLE OF INVENTION:  POLYCYSTIC KIDNEY DISEASE GENE
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  ONE MOUNTAIN ROAD
;      CITY:  FRAMINGHAM
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
```

```
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,136
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LASSEN, ELIZABETH
;      REGISTRATION NUMBER:  31,845
;      REFERENCE/DOCKET NUMBER:  GEN4-17.8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53526 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-658-136-2

  Query Match             1.0%;  Score 36;  DB 3;  Length 53526;
  Best Local Similarity   51.2%;  Pred. No. 26;
  Matches   84;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy     241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
           |||||  || | |    |   ||||||||   ||||| || ||   || ||     || |
Db   35344 AGGAGGGGGATGGGATGGGAGGAGGGAGGAGGGGAGGAGGGGGATGGGAGGAGGGGAGGA 35285

Qy     301 CGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
            | ||  |  |   ||||  |  || | ||   ||      || | |||| |   |||
Db   35284 GGGGGCATGGGAGGAGAGGAGGAGGAAGGAGGGGAGGAGAGGAGGGGGAATAGGAGGAGG 35225

Qy     361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGG 404
           | | |||||   ||  | |  | ||  ||  |  |   ||  ||
Db   35224 GGAGGAGAGGAGGGGGGATAGGAGGAGGGAAGGAGAGGAGGGGG 35181

RESULT 11
US-08-658-136-1/c
; Sequence 1, Application US/08658136
; Patent No. 6071717
;  GENERAL INFORMATION:
;    APPLICANT:  KLINGER, KATHERINE W
;    APPLICANT:  LANDES, GREGORY M
;    APPLICANT:  BURN, TIMOTHY C
;    APPLICANT:  CONNORS, TIMOTHY D
;    APPLICANT:  DACKOWSKI, WILLIAM
;    APPLICANT:  GERMINO, GREGORY
;    APPLICANT:  QIAN, FENG
;    TITLE OF INVENTION:  POLYCYSTIC KIDNEY DISEASE GENE
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  ONE MOUNTAIN ROAD
;      CITY:  FRAMINGHAM
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,136
;      FILING DATE:
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LASSEN, ELIZABETH
;      REGISTRATION NUMBER:  31,845
;      REFERENCE/DOCKET NUMBER:  GEN4-17.8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53577 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-658-136-1

  Query Match              1.0%;  Score 36;  DB 3;  Length 53577;
  Best Local Similarity   51.2%;  Pred. No. 26;
  Matches   84;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCGGGGAGGTGGCCCACAGAA 300
            |||||  || | |    |   ||||||||   ||||| || ||   || ||     || |
Db    35339 AGGAGGGGGATGGATGGAGGAGGGAGGAGGGGAGGAGGGGGATGGAGGAGGGGAGGA 35280

Qy      301 CGCGGGTTCTGTAAAGAGACGTTGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGATT 360
             | ||  |  |   ||||  |  || | ||   ||      || | |||| |   |||
Db    35279 GGGGGCATGGAGGAGAGGAGGAGGAAGGAGGGGAGGAGAGGAGGGGAATAGGAGGAGG 35220

Qy      361 GAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGG 404
            | | |||||   ||  | |  | ||  ||  |  |   ||  ||
Db    35219 GGAGGAGAGGAGGGGGGATAGGAGGAGGGAAGGAGAGGAGGGGG 35176

RESULT 12
US-09-118-442-26
; Sequence 26, Application US/09118442B
; Patent No. 6197561
; GENERAL INFORMATION:
;  APPLICANT: Martino-Catt, Susan J.
;  APPLICANT: Wang, Hongyu
;  APPLICANT: Beach, Larry R.
;  APPLICANT: Wang, Xun
;  APPLICANT: Bowen, Benjamin A.
;  TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
;  TITLE OF INVENTION: Plants and Uses Thereof
;  FILE REFERENCE: 0706
;  CURRENT APPLICATION NUMBER: US/09/118,442B
;  CURRENT FILING DATE: 1998-07-17
;  EARLIER APPLICATION NUMBER: 60/055,446
;  EARLIER FILING DATE: 1997-08-11
;  EARLIER APPLICATION NUMBER: 60/055,526
;  EARLIER FILING DATE: 1997-08-08
;  EARLIER APPLICATION NUMBER: 60/053,944
;  EARLIER FILING DATE: 1997-07-28
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(549)
;   OTHER INFORMATION: n = A,T,C or G
US-09-118-442-26

  Query Match              1.0%;  Score 35.8;  DB 4;  Length 549;
  Best Local Similarity   53.1%;  Pred. No. 1.3;
  Matches   76;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy     1551 TGCTTTATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGC 1610
            | || |   |||| || || ||||| || |||  |||||| ||    |||  |   ||||
Db      213 TCCTATTCTTTGGGATAATCGACATCCTCCAGGATTACAGCTTAAGAAAGCGGGCCGAGC 272

Qy     1611 ACTCTTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCT 1670
            |  |||  ||  |  |       ||     || |  |||| |       |||     |||
Db      273 ATGCTTACAAGTCATTACAGACAGATCCCAACTCGATCTCTGCCGTGGACCCGAAGCTCT 332

Qy     1671 ACGCTGAACGGTTCCAGCGCTTC 1693
            || |  |  | |||||   ||||
Db      333 ACTCGAAGAGTTTCCAAGACTTC 355

RESULT 13
US-09-677-064-26
; Sequence 26, Application US/09677064
; Patent No. 6291224
; GENERAL INFORMATION:
;  APPLICANT:  Martino-Catt, Susan J.
;  APPLICANT:  Wang, Hongyu
;  APPLICANT:  Beach, Larry R.
;  TITLE OF INVENTION:  Genes Controlling Phytate Metabolism in
;  TITLE OF INVENTION:  Plants and Uses Thereof
;  FILE REFERENCE:  0706D
;  CURRENT APPLICATION NUMBER: US/09/677,064
;  CURRENT FILING DATE:  2000-09-29
;  PRIOR APPLICATION NUMBER:  60/055,446
;  PRIOR FILING DATE:  1997-08-11
;  PRIOR APPLICATION NUMBER:  60/055,526
;  PRIOR FILING DATE:  1997-08-08
;  PRIOR APPLICATION NUMBER:  60/053,944
;  PRIOR FILING DATE:  1997-07-28
;  PRIOR APPLICATION NUMBER:  09/118,442
;  PRIOR FILING DATE:  1998-07-17
;  NUMBER OF SEQ ID NOS:  31
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 26
;   LENGTH: 549
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(549)
;   OTHER INFORMATION: n = A,T,C or G
US-09-677-064-26

  Query Match              1.0%;  Score 35.8;  DB 4;  Length 549;
  Best Local Similarity   53.1%;  Pred. No. 1.3;
  Matches   76;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy     1551 TGCTTTATATTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGC 1610
            | || |   |||| || || ||||| || |||  |||||| ||    |||  |   ||||
Db      213 TCCTATTCTTTGGGATAATCGACATCCTCCAGGATTACAGCTTAAGAAAGCGGGCCGAGC 272

Qy     1611 ACTCTTGGAAAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCT 1670
            |  |||  ||  |  |       ||     || |  |||| |       |||     |||
Db      273 ATGCTTACAAGTCATTACAGACAGATCCCAACTCGATCTCTGCCGTGGACCCGAAGCTCT 332

Qy     1671 ACGCTGAACGGTTCCAGCGCTTC 1693
            || |  |  | |||||   ||||
Db      333 ACTCGAAGAGTTTCCAAGACTTC 355

RESULT 14
US-09-134-001C-2534/c
; Sequence 2534, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
```

```
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2534
;   LENGTH: 1164
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2534

  Query Match              1.0%;  Score 35.8;  DB 4;  Length 1164;
  Best Local Similarity   49.7%;  Pred. No. 2.1;
  Matches   91;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy    957 AAGAGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACC 1016
          || |  | | | | |||||  | |   || |     ||||  |    ||    | |  ||
Db    759 AACAATCAGTAATACTGCACCATCATTTTTCTTACAACTATTTCCTACTGTGACTGTTCC 700

Qy   1017 CTCGGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACA 1076
           ||         ||  | || |||    | ||| ||| | | | |  |  |   |  ||
Db    699 TTCATTTAAAAGTGGTTTAAGTCTGCCAAGTGTTCTGAGAGTAAGTTGAGGTTTAATACT 640

Qy   1077 TTCGGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATG 1136
          |||   |||     |  |   | |||| ||   || |||||||| | | |   ||||||
Db    639 TTCATCTTGATTAAAATATTCACCTTTCACTTTGAACGGTAAAATTTCTTGGGAAATATT 580

Qy   1137 ACC 1139
          |||
Db    579 ACC 577

RESULT 15
US-09-072-596-323/c
; Sequence 323, Application US/09072596
; Patent No. 6458366
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    APPLICANT:  Skeiky, Yasir A.W.
;    APPLICANT:  Dillon, Davin C.
;    APPLICANT:  Campos-Neto, Antonia
;    APPLICANT:  Houghton, Raymond
;    APPLICANT:  Vedvick, Thomas S.
;    APPLICANT:  Twardzik, Daniel R.
;    APPLICANT:  Lodes, Michael J.
;    APPLICANT:  Hendrickson, Ronald C.
;    TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR DIAGNOSIS OF    TUBERCULOSIS
;    NUMBER OF SEQUENCES:  350
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/072,596
;      FILING DATE:  05-MAY-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.417C9
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  323:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1166 base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-09-072-596-323

  Query Match              1.0%;  Score 35.8;  DB 4;  Length 1166;
  Best Local Similarity   29.1%;  Pred. No. 2.1;
  Matches   83;  Conservative   54;  Mismatches  148;  Indels    0;  Gaps    0;

Qy    163 GCGGTTAAACTTGTGGAGGGGGTGCGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGT 222
          | ||  ||   || |::|: | :|:| :  ::        |::   |    |     :|
Db    559 GAGGGGAAKNMTGSGKRGKAGADGMGTSGGRKATNGGTGMCSMAGNGKTGAGRYGNGSGG 500

Qy    223 GTGGCCTTGAGCTGGTCCAGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCGGAGGGGGCG 282
          | ::    |: | ||     : |   ::: || | : |  |:|| ||   |  |: : :|
Db    499 GNKKANAGGWACCGGANKGARTGRGAKMKGGAGGGRRCNCARGGTGGNKTGAGGRCSCSG 440

Qy    283 GGGAGGTGGCCCACAGAACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAG 342
          :|: |:  | | |  |:  |: |:|:| |     :     |     :|:  :|  ||:::
Db    439 KGKGGRATGACGAGGGRTWGSMGRTWCGGGGGKNRAKTASTCCNNGRAKAGRASACCKMK 380

Qy    343 AAGAGGAAGAACCGGATTGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGAT 402
           |:  :: |  : |  :: |   :     :  ||| |: : ||:  ::::   | |   |
Db    379 SAKTTSMGGKSSAGNGKKAAGGAMCNAARWWNCCGTTSCSCGGRGTRRRSAACCSACATT 320

Qy    403 GGCGTCGGCCTCCTCCGGGCCGTCGTCTTCGGTCGGTTTTTCATC 447
            |||   |    |  :  ||  ||    ||||| | || |:| |
Db    319 CCCGTTACCGGTATTGRAACCACCGNACCCGGTCAGRTTRTYACC 275

Search completed: May 13, 2003, 02:16:52
Job time : 709 secs
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Qy       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TGCCTCGTTTTTTTTTCAGATGTGGCTTGGTCTGGGCGCAAGGTCCCAGCAGCCAGCTTA 120

Qy      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGCTTACTCTTCTGTGAAAGGGGAAAGTATCCCCTGTGGAAAGCGGTTAAACTTGTGGAG 180

Qy      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGGGTGCGGGACGTGAGTTCTTCCCCATGCCAGGCGAATGGTGTGGCCTTGAGCTGGTCC 240

Qy      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGG-CCCGGAGGGGGCGGGGAGGTGGCCCACAGA 299
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      241 AGGAGCCGGCTCGACGTGTCTGAGGGAGGCCCCGGAGGGGGCGGGGAGGTGGCCCACAGA 300

Qy      300 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ACGCGGGTTCTGTAAAGAGACGTTGGGAAGATTCGATTCCGAGAAGAGGAAGAACCGGAT 360

Qy      360 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 TGAAAGAGAGCCAGGCCGCTGAGGGGGAGGGGGCTGCTAAGATGGCGTCGGCCTCCTCCG 420

Qy      420 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGCCGTCGTCTTCGGTCGGTTTTTCATCCTTTGATCCCGCGGTCCCTTCCTGTACCTTGT 480

Qy      480 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CCTCAGCATCTGGAATCAAGAGACCCATGGCATCTGAGGTGCCTTATGCCTCTGGCATGC 540

Qy      540 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CCATCAAGAAAATAGGCCATAGAAGTGTTGATTCCTCAGGAGAGACAACATATAAAAAGA 600

Qy      600 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 659
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 CAACCTCATCAGCCTTGAAAGGTGCCATCCAGTTAGGCATTACCCACACTGTGGGGAGCC 660

Qy      660 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGAGTACCAAACCAGAGCGTGATGTCCTCATGCAAGATTTCTACGTGGTTGAGAGTATCT 720

Qy      720 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 779
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TCTTTCCCAGTGAAGGGAGCAACCTGACCCCTGCTCATCACTACAATGACTTTCGTTTCA 780

Qy      780 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 839
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AGACCTATGCACCTGTTGCCTTCCGCTACTTCCGGGAGCTATTTGGTATCCGGCCCGATG 840

Qy      840 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 899
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ATTACTTGTATTCCCTCTGCAGTGAGCCGCTGATTGAACTCTGTAGCTCTGGAGCTAGTG 900

Qy      900 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GTTCCCTATTCTATGTGTCCAGCGACGATGAGTTCATTATTAAGACAGTCCAACATAAAG 960

Qy      960 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1019
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AGGCGGAATTTCTGCAGAAGCTGCTTCCAGGATACTACATGAACCTCAACCAGAACCCTC 1020

Qy     1020 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1079
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GGACTTTGCTGCCTAAATTCTATGGACTGTACTGTGTGCAGGCAGGTGGCAAGAACATTC 1080

Qy     1080 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1139
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GGATTGTGGTGATGAACAATCTTTTACCAAGATCGGTAAAAATGCATATCAAATATGACC 1140
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Qy     1140 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TCAAAGGCTCAACCTACAAACGGCGGGCTTCCCAGAAAGAGCGAGAGAAGCCTCTTCCCA 1200

Qy     1200 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1259
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CATTTAAAGACCTAGACTTCTTACAAGACATCCCTGATGGTCTTTTTTTGGATGCTGACA 1260

Qy     1260 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 TGTACAACGCTCTCTGTAAGACCCTGCAGCGTGACTGTTTGGTGCTGCAGAGCTTCAAGA 1320

Qy     1320 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1379
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 TAATGGATTACAGCCTCTTGATGTCAATCCATAATATAGATCATGCACAACGAGAGCCCT 1380

Qy     1380 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1439
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TAAGCAGTGAAACACAGTACTCAGTTGATACTCGAAGACCGGCCCCCCAAAAGGCTCTGT 1440

Qy     1440 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1499
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 ATTCCACAGCCATGGAATCCATCCAGGGAGAGGCTCGACGGGGTGGTACCATGGAGACTG 1500

Qy     1500 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1559
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 ATGACCATATGGGTGGCATCCCTGCCCGGAATAGTAAAGGGGAAAGGCTTCTGCTTTATA 1560

Qy     1560 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1619
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 TTGGCATCATTGACATTCTACAGTCTTACAGGTTTGTTAAGAAGTTGGAGCACTCTTGGA 1620

Qy     1620 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1679
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 AAGCCCTGGTACATGACGGAGACACTGTCTCAGTGCATCGCCCAGGCTTCTACGCTGAAC 1680

Qy     1680 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1739
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681 GGTTCCAGCGCTTCATGTGCAACACAGTATTTAAGAAGATTCCCTTGAAGCCTTCTCCTT 1740

Qy     1740 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1799
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1741 CCAAAAAGTTTCGGTCTGGCTCATCTTTCTCTCGGCGAGCAGGCTCCAGTGGCAACTCCT 1800

Qy     1800 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1859
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1801 GCATTACTTACCAGCCATCGGTCTCTGGGGAACACAAGGCACAAGTGACAACAAAGGCAG 1860

Qy     1860 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1919
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 AAGTGGAGCCAGGCGTTCACCTTGGTCGTCCTGATGTTTTACCTCAGACTCCACCTTTGG 1920

Qy     1920 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1979
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 AGGAAATCAGTGAGGGCTCGCCTATTCCTGACCCCAGTTTCTCACCTCTAGTTGGAGAGA 1980

Qy     1980 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2039
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2040

Qy     2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2100

Qy     2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2160

Qy     2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2220

Qy     2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
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Db   2453 CTTTGCAAATGCTAACTACAAGTACAACCTTGGAAAAGCTTGAAGTTGCAGAGTCAGAGT 2512

Qy   2040 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2099
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Db   2513 TCACCCATTAAGCGCAAAGCCTCAGAAGACCTGGAACAAGATTCTGCCATCTCTGTGATC 2572

Qy   2100 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2573 CCAAGATGTCAGCCCTTGCCCCAGCAATGCTGAATTTTCTTCTACTTGGTCATCAAAAAA 2632

Qy   2160 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2633 GGAGTGTAATAGAAGTGAGGGGAGCTGCTCCTCCATCTTCTTCCTGAAGAAGAACCTTCT 2692

Qy   2220 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2693 CTCCTTCCTCTTCCTCATGAATGGGCCTTAGTGCCTCAGAGAGTTGAGGACCGCAGCATC 2752

Qy   2280 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2753 CCCTCCACTCCAGAGTTGGGTGGTACGGATTTTCAACTGGCCAACCCTTTGCCTCCACTA 2812

Qy   2340 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2813 TTGAATTTTTTTCAGACCCCCATTCTTCATGCTGGAAATGGGATTGCTGGACTTGGCAGC 2872

Qy   2400 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2873 TTTCTTTCCCCTCGTCTTTGACTAGGAACCGGACTCTTAATTTCCTCAGGACAGACTAGC 2932

Qy   2460 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2519
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Db   2933 TGGCACATTATCCCTACCTTAGTTCTTTCTCTCTGACTCCTGGAAGAATACTCCTGTAAT 2992

Qy   2520 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 2579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2993 CTCTGTAAAGGTTTTTGGGGGATAAGGGTGTTTAACCACCTCCCAGCTTTCTTCTTCTTT 3052

Qy   2580 TTTTTTTCTGAAAAAAGGAAAAAGCACACAGCACACAATTTCAAGCCATTTTCAGATCAG 2639
          |||||||    ||||| | |||| ||||||||||||||||||||||||||||||||||||
Db   3053 TTTTTTTTCTGAAAAAAGGAAAAACACACAGCACACAATTTCAAGCCATTTTCAGATCAG 3112

Qy   2640 AACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGT 2699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3113 AACTCCAGAAGTGTTGACAAGATGCCTATTCGTAGAGTTCCCTCAGAAGAGCCATGGTGT 3172

Qy   2700 TTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTC 2759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3173 TTATGAAGAGAAGAGTAGTGATTGCTCTGCCAGAAGCAGCTCCTCTTTAAACTCCTCCTC 3232

Qy   2760 TCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTAT 2819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3233 TCTTGATGAATTTCTTAAGGCTGAAGGAATGAAGAGAGTGGGACATGGGGTAATCTTTAT 3292

Qy   2820 CCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGA 2879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3293 CCCTTTTGTTAAAACAGGAGGCAGCCATGGGCTGGGAGATCATAGCCCTTCCTAGGCAGA 3352

Qy   2880 ATCCTGTTCACTGCCAGGCTATAGTAATTATTACTATTTTGCAATTTGAAATATATTCTG 2939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2940 GTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGAT 2999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3413 GTTGTTTTTCTAAATGTGAAGACTTACCAAATGAATTTTAGATCATTCTCCAGAGGAGAT 3472

Qy   3000 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAG 3059
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Db   3473 TTTTTTTGCTCTTCTCATCTTTTCCAACAGTGTTCTCCTGTTTGTGGAGCTAAGGTAAAG 3532

Qy   3060 AGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTC 3119
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Db   3533 AGGGGACACTTCTGTCTGTTTAACAGACAGTCCATATCTGTGAGGCCAGCAAATATTTTC 3592

Qy   3120 TTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGT 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3593 TTAAACTCATGGGGAGACAGCAGATTCTTGCCTTGGTGAGGTCATTGCTGTGCCATATGT 3652

Qy   3180 CCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTC 3239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3653 CCTACCCCCCTGTCTTCATGCAGGGAAGTTGGAAATGGGGGCTACATATGCCCTCTCCTC 3712

Qy   3240 CCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGG 3299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3713 CCCGTCTACAAGAGTTGTGGTTTTCCATCTGATCCTTCCACTCTTGTCAGGGGAAGAAGG 3772

Qy   3300 GGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCT 3359
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3773 GGGCCTGGTATCTCAGGCAGATTGTTGAATTCCTGTTCTATCCCTTCTCTATCCCACCCT 3832

Qy   3360 GCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCA 3419
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Db   3833 GCCTTGATAATATGTTAGCCCATACCCCAAATAACTGTCTATATTAGACACCCCCAGCCA 3892

Qy   3420 GTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTAT 3479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3893 GTTTCTGGCTGCCTGTCTTTGCTGCCATGTTTTTTACAAGAAGGAAAGAATTCTTGCTAT 3952

Qy   3480 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCT 3539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3953 TTTTTTTTCATAATTTACTATTTATGATGTATTTAAGTGTTTTATTAAGGACAGAGTTCT 4012

Qy   3540 GTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAG 3599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4013 GTTAGGGGTGGGAGGGAATATTTGAGGGAGGGCTGGGTCTTAGGGAAAGGAATGGGGAAG 4072

Qy   3600 CAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAAT 3659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4073 CAACATTTTTATTAAGTGTTACTATTTGCCTCTACTTTGTATTGTTCAGAAATGGCAAAT 4132

Qy   3660 ACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 3713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4133 ACAATATAAAAGTGATATATGGTTTTAATGTAATAAACTTTAATGAGTTATTTA 4186


RESULT 5
US-60-324-185-24985
; Sequence 24985, Application US/60324185
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE: GX-0019-1 P
;  CURRENT APPLICATION NUMBER: US/60/324,185
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 35862
;  SOFTWARE: PERL Program
; SEQ ID NO 24985
;   LENGTH: 3720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 348086.13
US-60-324-185-24985

  Query Match             99.3%;  Score 3688;  DB 76;  Length 3720;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3711;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    2;

Qy      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATTAACAGGCCGTGGTTAGGAAGGACGGAGAAGGGGCGTTCGCTCCTTTGGGACTTTTCA 60
```